

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
Zhong, Zhong
- (ii) TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Klauber & Jackson
 - (B) STREET: 411 Hackensack Avenue
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/212,185
 - (B) FILING DATE: 11-MAR-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/980,498
 - (B) FILING DATE: 23-NOV-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/854,296
 - (B) FILING DATE: 19-MAR-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO US93/02569
 - (B) FILING DATE: 19-MAR-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/126,588
 - (B) FILING DATE: 24-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 600-1-073 CIP
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201 487-5800
 - (B) TELEFAX: 201 343-1684
 - (C) TELEX: 133521

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (vii) IMMEDIATE SOURCE:
 (B) CLONE: HeLa
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 25..2577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | |
|---|-------------------------------------|-----|
| ACTGCAACCC TAATCAGAGC CCAA | ATG GCG CAG TGG GAA ATG CTG CAG AAT | 51 |
| | Met Ala Gln Trp Glu Met Leu Gln Asn | |
| | 1 5 | |
| CTT GAC AGC CCC TTT CAG GAT CAG CTG CAC CAG CTT TAC TCG CAC AGC | | 99 |
| Leu Asp Ser Pro Phe Gln Asp Gln Leu His Gln Leu Tyr Ser His Ser | | |
| 10 15 20 25 | | |
| CTC CTG CCT GTG GAC ATT CGA CAG TAC TTG GCT GTC TGG ATT GAA GAC | | 147 |
| Leu Leu Pro Val Asp Ile Arg Gln Tyr Leu Ala Val Trp Ile Glu Asp | | |
| 30 35 40 | | |
| CAG AAC TGG CAG GAA GCT GCA CTT GGG AGT GAT GAT TCC AAG GCT ACC | | 195 |
| Gln Asn Trp Gln Glu Ala Ala Leu Gly Ser Asp Asp Ser Lys Ala Thr | | |
| 45 50 55 | | |
| ATG CTA TTC TTC CAC TTC TTG GAT CAG CTG AAC TAT GAG TGT GGC CGT | | 243 |
| Met Leu Phe Phe His Phe Leu Asp Gln Leu Asn Tyr Glu Cys Gly Arg | | |
| 60 65 70 | | |
| TGC AGC CAG GAC CCA GAG TCC TTG TTG CTG CAG CAC AAT TTG CGG AAA | | 291 |
| Cys Ser Gln Asp Pro Glu Ser Leu Leu Leu Gln His Asn Leu Arg Lys | | |
| 75 80 85 | | |
| TTC TGC CGG GAC ATT CAG CCC TTT TCC CAG GAT CCT ACC CAG TTG GCT | | 339 |
| Phe Cys Arg Asp Ile Gln Pro Phe Ser Gln Asp Pro Thr Gln Leu Ala | | |
| 90 95 100 105 | | |
| GAG ATG ATC TTT AAC CTC CTT CTG GAA GAA AAA AGA ATT TTG ATC CAG | | 387 |
| Glu Met Ile Phe Asn Leu Leu Glu Glu Lys Arg Ile Leu Ile Gln | | |
| 110 115 120 | | |
| GCT CAG AGG GCC CAA TTG GAA CAA GGA GAG CCA GTT CTC GAA ACA CCT | | 435 |
| Ala Gln Arg Ala Gln Leu Glu Gln Gly Glu Pro Val Leu Glu Thr Pro | | |
| 125 130 135 | | |
| GTG GAG AGC CAG CAA CAT GAG ATT GAA TCC CGG ATC CTG GAT TTA AGG | | 483 |
| Val Glu Ser Gln Gln His Glu Ile Glu Ser Arg Ile Leu Asp Leu Arg | | |
| 140 145 150 | | |
| GCT ATG ATG GAG AAG CTG GTA AAA TCC ATC AGC CAA CTG AAA GAC CAG | | 531 |
| Ala Met Met Glu Lys Leu Val Lys Ser Ile Ser Gln Leu Lys Asp Gln | | |
| 155 160 165 | | |
| CAG GAT GTC TTC TGC TTC CGA TAT AAG ATC CAG GCC AAA GGG AAG ACA | | 579 |
| Gln Asp Val Phe Cys Phe Arg Tyr Lys Ile Gln Ala Lys Gly Lys Thr | | |
| 170 175 180 185 | | |

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|-------------------|-------------------|------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| CCC Pro | TCT Ser | CTG Leu | GAC Asp | CCC Pro 190 | CAT His | CAG Gln | ACC Thr | AAA Lys | GAG Glu 195 | CAG Gln | AAG Lys | ATT Ile | CTG Leu 200 | CAG Gln | GAA Glu | 627 |
| ACT Thr | CTC Leu | AAT Asn | GAA Glu 205 | CTG Leu | GAC Asp | AAA Lys | AGG Arg | AGA Arg 210 | AAG Lys | GAG Glu | GTG Val | CTG Leu | GAT Asp 215 | GCC Ala | TCC Ser | 675 |
| AAA Lys | GCA Ala | CTG Leu | CTA Leu 220 | GGC Gly | CGA Arg | TTA Leu | ACT Thr 225 | ACC Thr | CTA Leu | ATC Ile | GAG Glu | CTA Leu 230 | CTG Leu | CTG Leu | CCA Pro | 723 |
| AAG Lys | TTG Leu | GAG Glu | GAG Glu 235 | TGG Trp | AAG Lys | GCC Ala 240 | CAG Gln | CAG Gln | CAA Gln | AAA Lys | GCC Ala 245 | TGC Cys | ATC Ile | AGA Arg | GCT Ala | 771 |
| CCC Pro 250 | ATT Ile | GAC Asp | CAC His | GGG Gly 255 | TTG Leu | GAA Glu | CAG Gln | CTG Glu | GAG Leu | ACA Leu 260 | TGG Trp | TTC Phe | ACA Thr | GCT Thr | GGA Gly 265 | 819 |
| GCA Ala | AAG Lys | CTG Leu | TTG Leu | TTT Phe 270 | CAC His | CTG Leu | AGG Arg | CAG Gln | CTG Leu 275 | CTG Leu | AAG Lys | GAG Glu | CTG Leu | AAG Lys 280 | GGA Gly | 867 |
| CTG Leu | AGT Ser | TGC Cys | CTG Leu 285 | GTT Val | AGC Ser | TAT Tyr | CAG Gln | GAT Asp 290 | GAC Asp | CCT Pro | CTG Leu | ACC Thr | AAA Lys 295 | GGG Gly | GTG Val | 915 |
| GAC Asp | CTA Leu | CGC Arg | AAC Asn | GCC Ala 300 | CAG Gln | GTC Val | ACA Thr 305 | GAG Glu | TTG Leu | CTA Leu | CAG Gln | CGT Arg 310 | CTG Leu | CTC Leu | CAC His | 963 |
| AGA Arg | GCC Ala 315 | TTT Phe | GTG Val | GTA Val | GAA Glu | ACC Thr 320 | CAG Gln | CCC Pro | TGC Cys | ATG Met | CCC Pro 325 | CAA Gln | ACT Thr | CCC Pro | CAT His | 1011 |
| CGA Arg 330 | CCC Pro | CTC Leu | ATC Ile | CTC Leu 335 | AAG Lys | ACT Thr 335 | GGC Gly | AGC Ser | AAG Lys 340 | TTC Phe | ACC Thr | GTC Val | CGA Arg | ACA Thr | AGG Arg 345 | 1059 |
| CTG Leu | CTG Leu | GTG Val | AGA Arg | CTC Leu 350 | CAG Gln | GAA Glu | GGC Gly | AAT Asn | GAG Glu 355 | TCA Ser | CTG Leu | ACT Thr | GTG Val | GAA Glu 360 | GTC Val | 1107 |
| TCC Ser | ATT Ile | GAC Asp | AGG Arg 365 | AAT Asn | CCT Pro | CCT Pro | CAA Gln | TTA Leu 370 | CAA Gln | GGC Gly | TTC Phe | CGG Arg | AAG Lys 375 | TTC Phe | AAC Asn | 1155 |
| ATT Ile | CTG Leu | ACT Thr | TCA Ser 380 | AAC Asn | CAG Gln | AAA Lys | ACT Thr 385 | TTG Leu | ACC Thr | CCC Pro | GAG Glu | AAG Lys 390 | GGG Gly | CAG Gln | AGT Ser | 1203 |
| CAG Gln 395 | GGT Gly | TTG Leu | ATT Ile | TGG Trp | GAC Asp | TTT Phe 400 | GGT Gly | TAC Tyr | CTG Leu | ACT Thr | CTG Leu 405 | GTG Val | GAG Glu | CAA Gln | CGT Arg | 1251 |
| TCA Ser 410 | GGT Gly | GGT Gly | TCA Ser | GGA Gly 415 | AAG Lys | GGC Gly | AGC Ser | AAT Asn | AAG Lys 420 | GGG Gly | CCA Pro | CTA Leu | GGT Gly | GTG Val | ACA Thr 425 | 1299 |
| GAG Glu | GAA Glu | CTG Leu | CAC His | ATC Ile 430 | ATC Ile | AGC Ser | TTC Phe | ACG Thr | GTC Val 435 | AAA Lys | TAT Tyr | ACC Thr | TAC Tyr | CAG Gln 440 | GGT Gly | 1347 |
| CTG Leu | AAG Lys | CAG Gln | GAG Glu 445 | CTG Leu | AAA Lys | ACG Thr | GAC Asp | ACC Thr 450 | CTC Leu | CCT Pro | GTG Val | GTG Val | ATT Ile 455 | ATT Ile | TCC Ser | 1395 |

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|-----------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| —AAC Asn Met | ATG | AAC 460 | CAG Gln | CTC Leu | TCA Ser | ATT Ile | GCC 465 | TGG Ala | GCT Ala | TCA Ser | GTT Val | CTC Leu | TGG Trp | TTC Phe | AAT Asn | 1443 |
| TTG Leu | CTC 475 | AGC Ser | CCA Pro | AAC Asn | CTT Leu | CAG 480 | AAC Asn | CAG Gln | CAG Gln | TTC Phe | TTC 485 | TCC Ser | AAC Asn | CCC Pro | CCC Pro | 1491 |
| AAG 490 | GCC Ala | CCC Pro | TGG Trp | AGC Ser | TTG 495 | CTG Leu | GGC Leu | CCT Gly | GCT Pro | CTC Ala | AGT 500 | TGG Ser | CAG Trp | TTC Gln | TCC Phe | 1539 |
| TCC Ser | TAT Tyr | GTT Val | GGC Gly | CGA 510 | GGC Gly | CTC Leu | AAC Asn | TCA Ser | GAC 515 | CAG Gln | CTG Leu | AGC Ser | ATG Met | CTG 520 | AGA Arg | 1587 |
| AAC Trp | AAG Lys | CTG Leu | TTC Phe | GGG 525 | CAG Gly | AAC Asn | TGT Cys | AGG 530 | ACT Thr | GAG Glu | GAT Asp | CCA Pro | TTA Leu | TTG Leu | TCC Ser | 1635 |
| TGG Trp | GCT Ala | GAC Phe | TTC 540 | ACT Thr | ACT Lys | CGA Arg | GAG 545 | AGC Glu | CCT Pro | CCT Pro | GGC Gly | AAG 550 | TTA Lys | CCA Leu | TTC Phe | 1683 |
| TGG Trp | ACA Thr | TGG 555 | CTG Leu | GAC Asp | AAA Lys | ATT 560 | CTG Leu | GAG Glu | TTG Leu | GTA Val | CAT His | GAC 565 | CAC Gln | CTG Leu | AAG Lys | 1731 |
| GAT Asp | CTC Leu | TGG Trp | AAT Asn | GAT Asp | GGA 575 | CGC Gly | ATC Arg | ATG Ile | GGC Met | TTT Phe | GTG 580 | AGT Val | CGG Ser | AGC Arg | CAG Gln | 1779 |
| GAG Glu | CGC Arg | CGG Arg | CTG Leu | CTG 590 | AAG Lys | AAG Lys | ACC Thr | ATG Met | TCT Ser | GGC 595 | ACC Gly | TTT Thr | CTA Phe | CTG Leu | CGC Arg | 1827 |
| TTC Phe | AGT Ser | GAA Glu | TCG Ser | TCA Ser | GAA Glu | GGG Gly | GGC Gly | ATT 610 | ACC Ile | TGC Thr | TCC Cys | TGG Ser | GTG Trp | GAG Val | CAC Glu | 1875 |
| CAG Gln | GAT Asp | GAT 620 | GAC Asp | AAG Lys | GTG Val | CTC Leu | ATC Ile | TAC 625 | TCT Tyr | GTG Ser | CAA Val | CCG Gln | TAC Pro | ACG Tyr | AAG Thr | 1923 |
| GAG Glu | GTG Val | CTG 635 | CAG Leu | TCA Gln | CTC Ser | CCG Leu | CTG Pro | ACT 640 | GAA Leu | ATC Thr | ATC Glu | CGC Ile | CAT Arg | TAC His | CAG Tyr | 1971 |
| TTG Leu | CTC 650 | ACT Thr | GAG Glu | GAG Glu | AAT 655 | ATA Ile | CCT Pro | GAA Glu | AAC Asn | CCA Pro | CTG 660 | CGC Leu | TTC Arg | CTC Phe | TAT Leu | 2019 |
| CCC Pro | CGA Arg | ATC Ile | CCC Pro | CGG 670 | GAT Asp | GAA Glu | GCT Ala | TTT Phe | GGG 675 | TGC Gly | TAC Cys | TAC Tyr | CAG Tyr | GAG Gln | AAA Lys | 2067 |
| GTT Val | AAT Asn | CTC Leu | CAG Gln | GAA 685 | CGG Glu | AGG Arg | AAA Lys | TAC 690 | CTG Tyr | AAA Leu | CAC Lys | AGG His | CTC Arg | ATT Leu | GTG Ile | 2115 |
| GTC Val | TCT Ser | AAT 700 | AGA Asn | CAG Gln | GTG Val | GAT Asp | GAA 705 | CTG Glu | CAA Gln | CAA Gln | CCG Pro | CTG 710 | GAG Glu | CTT Leu | AAG Lys | 2163 |
| CCA Pro | GAG Glu | CCA 715 | GAG Pro | CTG Glu | GAG Glu | TCA Ser | TTA 720 | GAG Leu | CTG Glu | GAA Glu | CTA 725 | GGG Gly | CTG Leu | GTG Val | CCA Pro | 2211 |

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|---|--|------|
| — | GAG CCA GAG CTC AGC CTG GAC TTA GAG CCA CTG CTG AAG GCA GGG CTG | 2259 |
| | Glu Pro Glu Leu Ser Leu Asp Leu Glu Pro Leu Lys Ala Gly Leu | |
| | 730 735 740 745 | |
| | GAT CTG GGG CCA GAG CTA GAG TCT GTG CTG GAG TCC ACT CTG GAG CCT | 2307 |
| | Asp Leu Gly Pro Glu Leu Glu Ser Val Leu Glu Ser Thr Leu Glu Pro | |
| | 750 755 760 | |
| | GTG ATA GAG CCC ACA CTA TGC ATG GTA TCA CAA ACA GTG CCA GAG CCA | 2355 |
| | Val Ile Glu Pro Thr Leu Cys Met Val Ser Gln Thr Val Pro Glu Pro | |
| | 765 770 775 | |
| | GAC CAA GGA CCT GTA TCA CAG CCA GTG CCA GAG CCA GAT TTG CCC TGT | 2403 |
| | Asp Gln Gly Pro Val Ser Gln Pro Val Pro Glu Pro Asn Leu Pro Cys | |
| | 780 785 790 | |
| | GAT CTG AGA CAT TTG AAC ACT GAG CCA ATG GAA ATC TTC AGA AAC TGT | 2451 |
| | Asp Leu Arg His Leu Asn Thr Glu Pro Met Glu Ile Phe Arg Asn Cys | |
| | 795 800 805 | |
| | GTA AAG ATT GAA GAA ATC ATG CCG AAT GGT GAC CCA CTG TTG GCT GGC | 2499 |
| | Val Lys Ile Glu Glu Ile Met Pro Asn Gly Asp Pro Leu Leu Ala Gly | |
| | 810 815 820 825 | |
| | CAG AAC ACC GTG GAT GAG GTT TAC GTC TCC CGC CCC AGC CAC TTC TAC | 2547 |
| | Gln Asn Thr Val Asp Glu Val Tyr Val Ser Arg Pro Ser His Phe Tyr | |
| | 830 835 840 | |
| | ACT GAT GGA CCC TTG ATG CCT TCT GAC TTC TAGGAACCAC ATTTCTCTCTG | 2597 |
| | Thr Asp Gly Pro Leu Met Pro Ser Asp Phe | |
| | 845 850 | |
| | TTCTTTTCAT ATCTCTTTGC CCTTCCTACT CCTCATAGCA TGATAATTGT CTCCAAGGAT | 2657 |
| | GGGAATCAGG CATGTGTCCC TTCCAAGCTG TGTTAACTGT TCAAACCTCAG GCCTGTGTGA | 2717 |
| | CTCCATTGGG GTGAGAGGTG AAAGCATAAC ATGGGTACAG AGGGGACAAC AATGAATCAG | 2777 |
| | AACAGATGCT GAGCCATAGG TCTAAATAGG ATCCTGGAGG CTGCCTGCTG TGCTGGGAGG | 2837 |
| | TATAGGGGTC CTGGGGGCAG GCCAGGGCAG TTGACAGSTA CTGGAGGGC TCAGGGCAGT | 2897 |
| | GGCTTCTTTC CAGTATGGAA GGATTTCAAC ATTTTAATAG TTGGTTAGGC TAAACTGGTG | 2957 |
| | CATACTGGCA TTGGCCTTGG TGGGGAGCAC AGACACAGGA TAGGACTCCA TTTCTTTCTT | 3017 |
| | CCATTCCTTC ATGTCTAGGA TAACTTGCTT TCTTCTTTCC TTTACTCCTG GCTCAAGCCC | 3077 |
| | TGAATTTCTT CTTTTCTGCG AGGGGTTGAG AGCTTTCTGC CTTAGCCTAC CATGTGAAAC | 3137 |
| | TCTACCTGA AGAAAGGGAT GGATAGGAAG TAGACCTCTT TTTCTTACCA GTCTCCTCCC | 3197 |
| | CTACTCTGCC CCTTAAGCTG GCTGTACCTG TTCTTCCCC ATAAAATGAT CCTGCCAATC | 3257 |
| | TAAAAAAA A | 3268 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 851 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Gln Trp Glu Met Leu Gln Asn Leu Asp Ser Pro Phe Gln Asp
 1 5 10 15
 Gln Leu His Gln Leu Tyr Ser His Ser Leu Leu Pro Val Asp Ile Arg
 20 25 30
 Gln Tyr Leu Ala Val Trp Ile Glu Asp Gln Asn Trp Gln Glu Ala Ala
 35 40 45
 Leu Gly Ser Asp Asp Ser Lys Ala Thr Met Leu Phe Phe His Phe Leu
 50 55 60
 Asp Gln Leu Asn Tyr Glu Cys Gly Arg Cys Ser Gln Asp Pro Glu Ser
 65 70 75 80
 Leu Leu Leu Gln His Asn Leu Arg Lys Phe Cys Arg Asp Ile Gln Pro
 85 90 95
 Phe Ser Gln Asp Pro Thr Gln Leu Ala Glu Met Ile Phe Asn Leu Leu
 100 105 110
 Leu Glu Glu Lys Arg Ile Leu Ile Gln Ala Gln Arg Ala Gln Leu Glu
 115 120 125
 Gln Gly Glu Pro Val Leu Glu Thr Pro Val Glu Ser Gln Gln His Glu
 130 135 140
 Ile Glu Ser Arg Ile Leu Asp Leu Arg Ala Met Met Glu Lys Leu Val
 145 150 155
 Lys Ser Ile Ser Gln Leu Lys Asp Gln Gln Asp Val Phe Cys Phe Arg
 165 170 175
 Tyr Lys Ile Gln Ala Lys Gly Lys Thr Pro Ser Leu Asp Pro His Gln
 180 185 190
 Thr Lys Glu Gln Lys Ile Leu Gln Glu Thr Leu Asn Glu Leu Asp Lys
 195 200 205
 Arg Arg Lys Glu Val Leu Asp Ala Ser Lys Ala Leu Leu Gly Arg Leu
 210 215 220
 Thr Thr Leu Ile Glu Leu Leu Leu Pro Lys Leu Glu Glu Trp Lys Ala
 225 230 235 240
 Gln Gln Gln Lys Ala Cys Ile Arg Ala Pro Ile Asp His Gly Leu Glu
 245 250 255
 Gln Leu Glu Thr Trp Phe Thr Ala Gly Ala Lys Leu Leu Phe His Leu
 260 265 270
 Arg Gln Leu Leu Lys Glu Leu Lys Gly Leu Ser Cys Leu Val Ser Tyr
 275 280 285
 Gln Asp Asp Pro Leu Thr Lys Gly Val Asp Leu Arg Asn Ala Gln Val
 290 295 300
 Thr Glu Leu Leu Gln Arg Leu Leu His Arg Ala Phe Val Val Glu Thr
 305 310 315 320
 Gln Pro Cys Met Pro Gln Thr Pro His Arg Pro Leu Ile Leu Lys Thr
 325 330 335
 Gly Ser Lys Phe Thr Val Arg Thr Arg Leu Leu Val Arg Leu Gln Glu
 340 345 350
 Gly Asn Glu Ser Leu Thr Val Glu Val Ser Ile Asp Arg Asn Pro Pro
 355 360 365

Gln Leu Gln Gly Phe Arg Lys Phe Asn Ile Leu Thr Ser Asn Gln Lys
 370 375 380
 Thr Leu Thr Pro Glu Lys Gly Gln Ser Gln Gly Leu Ile Trp Asp Phe
 385 390 395 400
 Gly Tyr Leu Thr Leu Val Glu Gln Arg Ser Gly Gly Ser Gly Lys Gly
 405 410 415
 Ser Asn Lys Gly Pro Leu Gly Val Thr Glu Glu Leu His Ile Ile Ser
 420 425 430
 Phe Thr Val Lys Tyr Thr Tyr Gln Gly Leu Lys Gln Glu Leu Lys Thr
 435 440 445
 Asp Thr Leu Pro Val Val Ile Ile Ser Asn Met Asn Gln Leu Ser Ile
 450 455 460
 Ala Trp Ala Ser Val Leu Trp Phe Asn Leu Leu Ser Pro Asn Leu Gln
 465 470 475 480
 Asn Gln Gln Phe Phe Ser Asn Pro Pro Lys Ala Pro Trp Ser Leu Leu
 485 490 495
 Gly Pro Ala Leu Ser Trp Gln Phe Ser Ser Tyr Val Gly Arg Gly Leu
 500 505 510
 Asn Ser Asp Gln Leu Ser Met Leu Arg Asn Lys Leu Phe Gly Gln Asn
 515 520 525
 Cys Arg Thr Glu Asp Pro Leu Leu Ser Trp Ala Asp Phe Thr Lys Arg
 530 535 540
 Glu Ser Pro Pro Gly Lys Leu Pro Phe Trp Thr Trp Leu Asp Lys Ile
 545 550 555 560
 Leu Glu Leu Val His Asp His Leu Lys Asp Leu Trp Asn Asp Gly Arg
 565 570 575
 Ile Met Gly Phe Val Ser Arg Ser Gln Glu Arg Arg Leu Leu Lys Lys
 580 585 590
 Thr Met Ser Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Glu Gly
 595 600 605
 Gly Ile Thr Cys Ser Trp Val Glu His Gln Asp Asp Lys Val Leu
 610 615 620
 Ile Tyr Ser Val Gln Pro Tyr Thr Lys Glu Val Leu Gln Ser Leu Pro
 625 630 635 640
 Leu Thr Glu Ile Ile Arg His Tyr Gln Leu Leu Thr Glu Glu Asn Ile
 645 650 655
 Pro Glu Asn Pro Leu Arg Phe Leu Tyr Pro Arg Ile Pro Arg Asp Glu
 660 665 670
 Ala Phe Gly Cys Tyr Tyr Gln Glu Lys Val Asn Leu Gln Glu Arg Arg
 675 680 685
 Lys Tyr Leu Lys His Arg Leu Ile Val Val Ser Asn Arg Gln Val Asp
 690 695 700
 Glu Leu Gln Gln Pro Leu Glu Leu Lys Pro Glu Pro Glu Leu Glu Ser
 705 710 715 720
 Leu Glu Leu Glu Leu Gly Leu Val Pro Glu Pro Glu Leu Ser Leu Asp
 725 730 735

Leu Glu Pro Leu Leu Lys Ala Gly Leu Asp Leu Gly Pro Glu Leu Glu
 740 745 750
 Ser Val Leu Glu Ser Thr Leu Glu Pro Val Ile Glu Pro Thr Leu Cys
 755 760 765
 Met Val Ser Gln Thr Val Pro Glu Pro Asp Gln Gly Pro Val Ser Gln
 770 775 780
 Pro Val Pro Glu Pro Asp Leu Pro Cys Asp Leu Arg His Leu Asn Thr
 785 790 795 800
 Glu Pro Met Glu Ile Phe Arg Asn Cys Val Lys Ile Glu Glu Ile Met
 805 810 815
 Pro Asn Gly Asp Pro Leu Leu Ala Gly Gln Asn Thr Val Asp Glu Val
 820 825 830
 Tyr Val Ser Arg Pro Ser His Phe Tyr Thr Asp Gly Pro Leu Met Pro
 835 840 845
 Ser Asp Phe
 850

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3943 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Human Stat91
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 197..2449
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|---|-----|
| ATTAAACCTC TCGCCGAGCC CTTCCGCAGA CTCGCGCCG GAAAGTTTCA TTGCTGTAT | 60 |
| GCCATCCTCG AGAGCTGTCT AGGTTAACGT TCGACTCTG TGTATATAAC CTCGACAGTC | 120 |
| TTGGCACCTA ACGTGCTGTG CGTAGCTGCT CCTTTGGTTG AATCCCCAGG CCCTTGTTGG | 180 |
| GGCACAAGGT GGCAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC | 229 |
| Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp | |
| 1 5 10 | |
| TCA AAA TTC CTG GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC | 277 |
| Ser Lys Phe Leu Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro | |
| 15 20 25 | |
| ATG GAA ATC AGA CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG | 325 |
| Met Glu Ile Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp | |
| 30 35 40 | |

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|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| GAG Glu | CAC His | GCT Ala | GCC Ala | AAT Asn | GAT Asp | GTT Val | TCA Ser | TTT Phe | GCC Ala | ACC Thr | ATC Ile | CGT Arg | TTT Phe | CAT His | GAC Asp | 373 |
| CTC Leu | CTG Leu | TCA Ser | CAG Gln | CTG Leu | GAT Asp | GAT Asp | CAA Gln | TAT Tyr | AGT Ser | CGC Arg | TTT Phe | TCT Ser | TTG Leu | GAG Glu | AAT Asn | 421 |
| AAC Asn | TTC Phe | TTG Leu | CTA Leu | CAG Gln | CAT His | AAC Asn | ATA Ile | AGG Arg | AAA Lys | AGC Ser | AAG Lys | CGT Arg | AAT Asn | CTT Gln | CAG Gln | 469 |
| GAT Asp | AAT Asn | TTT Phe | CAG Gln | GAA Glu | GAC Asp | CCA Pro | ATC Ile | CAG Gln | ATG Met | TCT Ser | ATG Met | ATC Ile | ATT Ile | TAC Tyr | AGC Ser | 517 |
| TGT Cys | CTG Leu | AAG Lys | GAA Glu | GAA Glu | AGG Arg | AAA Lys | ATT Ile | CTG Leu | GAA Glu | AAC Asn | GCC Ala | CAG Gln | AGA Arg | TTT Phe | AAT Asn | 565 |
| CAG Gln | GCT Ala | CAG Gln | TCG Ser | GGG Gly | AAT Asn | ATT Ile | CAG Gln | AGC Ser | ACA Thr | GTG Val | ATG Met | TTA Leu | GAC Asp | AAA Lys | CAG Gln | 613 |
| AAA Lys | GAG Glu | CTT Leu | GAC Asp | AGT Ser | AAA Lys | GTC Val | AGA Arg | AAT Asn | GTG Val | AAG Lys | AAG Asp | GTT Lys | ATG Val | TGT Met | Cys Lys | 661 |
| ATA Ile | GAG Glu | CAT His | GAA Glu | ATC Ile | AAG Lys | AGC Ser | CTG Leu | GAA Glu | GAT Asp | TTA Leu | CAA Gln | GAT Asp | GAA Glu | TAT Tyr | GAC Asp | 709 |
| TTC Phe | AAA Lys | TGC Cys | AAA Lys | ACC Thr | TTG Leu | CAG Gln | AAC Asn | AGA Arg | GAA Glu | CAC His | GAG Glu | ACC Thr | AAT Asn | GGT Gly | GTG Val | 757 |
| GCA Ala | AAG Lys | AGT Met | GAT Ser | CAG Gln | AAA Lys | CAA Gln | GAA Glu | CAG Gln | CTG Leu | TTA Leu | CTC Leu | AAG Lys | AAG Lys | ATG Met | TAT Tyr | 805 |
| TTA Leu | ATG Met | CTT Leu | GAC Asp | AAT Asn | AAG Lys | AGA Arg | AAG Lys | GAA Glu | GTA Val | GTT Val | CAC His | AAA Lys | ATA Ile | ATA Ile | GAG Glu | 853 |
| TTG Leu | CTG Leu | AAT Asn | GTC Val | ACT Thr | GAA Glu | CTT Leu | ACC Thr | CAG Gln | AAT Asn | GCC Ala | CTG Leu | ATT Ile | AAT Asn | GAT Asp | GAA Glu | 901 |
| CTA Leu | GTG Val | GAG Glu | TGG Trp | AAG Lys | CGG Arg | AGA Arg | CAG Gln | CAG Gln | AGC Ser | GCC Ala | TGT Cys | ATT Ile | GGG Gly | GGG Pro | CCG Pro | 949 |
| CCC Pro | AAT Asn | GCT Ala | TGC Cys | TTG Leu | GAT Asp | CAG Gln | CTG Leu | CAG Gln | AAC Asn | TGG Trp | TTC Phe | ACT Thr | ATA Ile | GTT Val | GCG Ala | 997 |
| GAG Glu | AGT Ser | CTG Leu | CAG Gln | CAA Gln | GTT Val | CGG Arg | CAG Gln | CAG Gln | CTT Leu | AAA Lys | AAG Lys | TTG Lys | GAG Glu | GAA Glu | TTG Leu | 1045 |
| GAA Glu | CAG Gln | AAA Lys | TAC Tyr | ACC Thr | TAC Tyr | GAA Glu | CAT His | GAC Asp | CCT Pro | ATC Ile | ACA Lys | AAA Lys | AAC Asn | AAA Lys | CAA Gln | 1093 |
| GTG Val | TTA Leu | TGG Trp | GAC Asp | CGC Arg | ACC Thr | TTC Phe | AGT Ser | CTT Leu | TTC Phe | CAG Gln | CAG Gln | CTC Leu | ATT Ile | CAG Gln | AGC Ser | 1141 |

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|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| TCG Ser | TTT Phe | GTG Val | GTG Val | GAA Glu 320 | AGA Arg | CAG Gln | CCC Pro | TGC Cys | ATG Met 325 | CCA Pro | ACG Thr | CAC His | CCT Pro | CAG Gln 330 | AGG Arg | 1189 |
| CCG Pro | CTG Leu | GTC Val | TTG Leu 335 | AAG Lys | ACA Thr | GGG Gly | GTC Val | CAG Gln 340 | TTC Phe | ACT Thr | GTG Val | AAG Lys | TTG Leu 345 | AGA Arg | CTG Leu | 1237 |
| TTG Leu | GTG Val | AAA Lys 350 | TTG Leu | CAA Gln | GAG Glu | CTG Leu | AAT Asn 355 | TAT Tyr | AAT Asn | TTG Leu | AAA Lys 360 | GTC Val 360 | AAA Lys | GTC Val | TTA Leu | 1285 |
| TTT Phe | GAT Asp 365 | AAA Lys | GAT Asp | GTG Val | AAT Asn | GAG Glu 370 | AGA Arg | AAT Asn | ACA Thr | GTA Val | AAA Lys 375 | GGA Gly | TTT Phe | AGG Arg | AAG Lys | 1333 |
| TTT Phe 380 | AAC Asn | ATT Ile | TTG Leu | GGC Gly | ACG Thr 385 | CAC His | ACA Thr | AAA Lys | GTG Val | ATG Met 390 | AAC Asn | ATG Met | GAG Glu | GAG Glu | TCC Ser 395 | 1381 |
| ACC Thr | AAT Asn | GGC Gly | AGT Ser | CTG Leu 400 | GCG Ala | GCT Ala | GAA Glu | TTT Phe | CGG Arg 405 | CAC His | CTG Leu | CAA Gln | TTG Leu | AAA Lys 410 | GAA Glu | 1429 |
| CAG Gln | AAA Lys | AAT Asn | GCT Ala 415 | GGC Gly | ACC Thr | AGA Arg | ACG Thr | AAT Asn 420 | GAG Glu | GGT Gly | CCT Pro | CTC Leu | ATC Ile 425 | GTT Val | ACT Thr | 1477 |
| GAA Glu | GAG Glu | CTT Leu 430 | CAC His | TCC Ser | CTT Leu | AGT Ser | TTT Phe 435 | GAA Glu | ACC Thr | CAA Gln | TTG Gly | TGC Leu 440 | CAG Gln | CCT Pro | GGT Gly | 1525 |
| TTG Leu | GTA Val 445 | ATT Ile | GAC Asp | CTC Glu | GAG Glu | ACG Thr 450 | ACC Thr | TCT Ser | CTG Pro | CCC Pro | GTT Val 455 | GTG Val | GTG Val | ATC Ile | TCC Ser | 1573 |
| AAC Asn 460 | GTC Val | AGC Ser | CAG Gln | CTC Leu | CCG Pro 465 | AGC Ser | GGT Gly | TGG Trp | GCC Ala | TCC Ser 470 | ATC Ile | CTT Leu | TGG Trp | TAC Tyr | AAC Asn 475 | 1621 |
| ATG Met | CTG Leu | GTG Val | GCG Ala | GAA Glu 480 | CCC Pro | AGG Arg | AAT Asn | CTG Ser | TCC Phe 485 | TTC Phe | TTC Phe | CTG Thr | ACT Thr | CCA Pro 490 | CCA Pro | 1669 |
| TGT Cys | GCA Ala | CGA Arg | TGG Trp 495 | GCT Ala | CAG Gln | CTT Leu | TCA Ser | GAA Glu 500 | GTG Val | CTG Leu | AGT Ser | TGG Trp | CAG Gln 505 | TTT Phe | TCT Ser | 1717 |
| TCT Ser | GTC Val | ACC Thr 510 | AAA Lys | AGA Arg | GGT Gly | CTC Leu | AAT Asn 515 | GTG Val | GAC Gln | CAG Gln | CTG Leu | AAC Asn 520 | ATC Met | TTG Leu | GGA Gly | 1765 |
| GAG Glu | AAG Lys 525 | CTT Leu | CTT Leu | GGT Gly | CCT Pro | AAC Asn 530 | GCC Ala | AGC Ser | CCC Pro | GAT Asp | GGT Gly 535 | CTC Leu | ATT Ile | CCG Pro | TGG Trp | 1813 |
| ACG Thr 540 | AGG Arg | TTT Phe | TGT Cys | AAG Lys | GAA Glu 545 | AAT Asn | ATA Ile | AAT Asn | GAT Asp | AAA Lys 550 | AAT Asn | TTT Phe | CCC Pro | TTC Phe | TGG Trp 555 | 1861 |
| CTT Leu | TGG Trp | ATT Ile | GAA Glu | AGC Ser | ATC Ile | CTA Leu | GAA Glu | CTC Leu | ATT Ile 565 | AAA Lys | AAA Lys | CAC His | CTG Leu | CTC Leu 570 | CCT Pro | 1909 |
| CTC Leu | TGG Trp | AAT Asn | GAT Asp 575 | GGG Gly | TGC Cys | ATC Ile | ATG Met | GGC Gly 580 | TTC Phe | ATC Ile | AGC Ser | AAG Lys | GAG Glu 585 | CGA Arg | GAG Glu | 1957 |

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|---|------|
| CGT GCC CTG TTG AAG GAC CAG CAG CCG GGG ACC TTC CTG CTG CGG TTC | 2005 |
| Arg Ala Leu Leu Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe | |
| 590 595 600 | |
| AGT GAG AGC TCC CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAG CGG | 2053 |
| Ser Glu Ser Ser Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg | |
| 605 610 615 | |
| TCC CAG AAC GGA GGC GAA CCT GAC TTC CAT GCG GTT GAA CCC TAC ACG | 2101 |
| Ser Gln Asn Gly Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr | |
| 620 625 630 635 | |
| AAG AAA GAA CTT TCT GCT GTT ACT TTC CCT GAC ATC ATT CGC AAT TAC | 2149 |
| Lys Lys Glu Leu Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr | |
| 640 645 650 | |
| AAA GTC ATG GCT GCT GAG AAT ATT CCT GAG AAT CCC CTG AAG TAT CTG | 2197 |
| Lys Val Met Ala Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu | |
| 655 660 665 | |
| TAT CCA AAT ATT GAC AAA GAC CAT GCC TTT GGA AAG TAT TAC TCC AGG | 2245 |
| Tyr Pro Asn Ile Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg | |
| 670 675 680 | |
| CCA AAG GAA GCA CCA GAG CCA ATG GAA CTT GAT GGC CCT AAA GGA ACT | 2293 |
| Pro Lys Glu Ala Pro Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr | |
| 685 690 695 | |
| GGA TAT ATC AAG ACT GAG TTG ATT TCT GTG TCT GAA GTT CAC CCT TCT | 2341 |
| Gly Tyr Ile Lys Thr Glu Leu Ile Ser Val Ser Glu Val His Pro Ser | |
| 700 705 710 715 | |
| AGA CTT CAG ACC ACA GAC AAC CTG CTC CCC ATG TCT CCT GAG GAG TTT | 2389 |
| Arg Leu Gln Thr Thr Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe | |
| 720 725 730 | |
| GAC GAG GTG TCT CGG ATA GTG GGC TCT GTA GAA TTC GAC AGT ATG ATG | 2437 |
| Asp Glu Val Ser Arg Ile Val Gly Ser Val Glu Phe Asp Ser Met Met | |
| 735 740 745 | |
| AAC ACA GTA TAGAGCATGA ATTTTTTTCA TCTTCTCTGG CGACAGTTTT | 2486 |
| Asn Thr Val 750 | |
| CCTTCTCATC TGTGATTCCC TCCTGCTACT CTGTTCCTTC ACATCCTGTG TTTCTAGGGA | 2546 |
| AATGAAAGAA AGGCCAGCAA ATTCGCTGCA ACCTGTTGAT AGCAAGTGAA TTTTCTCTA | 2606 |
| ACTCAGAAAC ATCAGTTACT CTGAAGGGCA TCATGCATCT TACTGAAGGT AAAATTGAAA | 2666 |
| GGCATTCTCT GAAGAGTGGG TTTCACAAGT GAAAAACATC CAGATACACC CAAAGTATCA | 2726 |
| GGACGAGAAT GAGGTCCTT TGGGAAAGGA GAAGTTAAGC AACATCTAGC AAATGTTATG | 2786 |
| CATAAAGTCA GTGCCCAACT GTTATAGGTT GTTGGATAAA TCAGTGGTTA TTTAGGGAAC | 2846 |
| TGCTTGACGT AGGAACGGTA AATTTCTGTG GGAGAATTCT TACATGTTTT CTTTGCTTTA | 2906 |
| AGTGTAACTG GCAGTTTTC ATTGGITTAC CTGTGAAATA GTTCAAAGCC AAGTTTATAT | 2966 |
| ACAATTATAT CAGTCCTCTT TCAAAGGTAG CCATCATGGA TCTGGTAGGG GGAATGTG | 3026 |
| TATTTTATTA CATCTTTTAC ATTGGCTATT TAAAGACAAA GACAAATCTT GTTCTTGAG | 3086 |
| AAGAGAACAT TTCCAAATTC ACAAGTTGTG TTTGATATCC AAAGCTGAAT ACATTCTGCT | 3146 |
| TTCACTCTGG TCACATACAA TTATTTTAC AGTCTCTCCA AGGGAGTTAG GCTATTACAC | 3206 |
| ACCACTCATT CAAAAGTTGA AATTAACCAT AGATGTAGAT AAACCTCAGAA ATTTAATTC | 3266 |

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|---|------|
| — TGTTCTTAA ATGGGCTACT TGTCCITTT TGTATTAGG GTGGTATTTA GTCTATTAGC | 3326 |
| CACAAAATTG GGAAAGGAGT AGAAAAAGCA GTAACGTACA ACTTGAATAA TACACCAGAG | 3386 |
| ATAATATGAG AATCAGATCA TTCAAACCT CATTTCCTAT GTAACGTGAT TGAGAACTGC | 3446 |
| ATATGTTTCG CTGATATATG TGTITTTTAC ATTTGCGAAT GGTTCCTTC TCTCTCTGT | 3506 |
| ACTTTTCCCA GACACTTTTT TGAGTGGATG ATGTTTCGTG AAGTATACTG TATTTTACC | 3566 |
| TTTTTCCTTC CTTATCACTG ACACAAAAAG TAGATTAAGA GATGGGTTTG ACAAGGTTCT | 3626 |
| TCCCTTTTAC ATACGTCTGT CTATGTGGCT GTATCTTGT TTTCCACTAC TGCTACCACA | 3686 |
| ACTATATTAT CATGCAAAAG CTGTATTCTT CTTTGGTGGA GATAAGATT TCTTGAGTTT | 3746 |
| TGTTTTAAAA TTAAGCTAA AGTATCTGTA TTGCATTAAA TATAATATCG ACACAGTGCT | 3806 |
| TTCCGTGGCA CTGCATACAA TCTGAGGCCT CCTCTCTCAG TTTTATATA GATGGCGAGA | 3866 |
| ACCTAAGTTT CAGTTGATTT TACAATTGAA ATGACTAAAA AACAAGAAG ACAACATTAA | 3926 |
| AAACAATATT GTTTCTA | 3943 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Trp | Tyr | Glu | Leu | Gln | Gln | Leu | Asp | Ser | Lys | Phe | Leu | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gln | Val | His | Gln | Leu | Tyr | Asp | Asp | Ser | Phe | Pro | Met | Glu | Ile | Arg | Gln |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Leu | Ala | Gln | Trp | Leu | Glu | Lys | Gln | Asp | Trp | Glu | His | Ala | Ala | Asn |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asp | Val | Ser | Phe | Ala | Thr | Ile | Arg | Phe | His | Asp | Leu | Leu | Ser | Gln | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Asp | Asp | Gln | Tyr | Ser | Arg | Phe | Ser | Leu | Glu | Asn | Asn | Phe | Leu | Leu | Gln |
| | 65 | | | | 70 | | | | | 75 | | | | 80 | |
| His | Asn | Ile | Arg | Lys | Ser | Lys | Arg | Asn | Leu | Gln | Asp | Asn | Phe | Gln | Glu |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Asp | Pro | Ile | Gln | Met | Ser | Met | Ile | Ile | Tyr | Ser | Cys | Leu | Lys | Glu | Glu |
| | | | 100 | | | | 105 | | | | | | 110 | | |
| Arg | Lys | Ile | Leu | Glu | Asn | Ala | Gln | Arg | Phe | Asn | Gln | Ala | Gln | Ser | Gly |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Asn | Ile | Gln | Ser | Thr | Val | Met | Leu | Asp | Lys | Gln | Lys | Glu | Leu | Asp | Ser |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Lys | Val | Arg | Asn | Val | Lys | Asp | Lys | Val | Met | Cys | Ile | Glu | His | Glu | Ile |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 |
| Lys | Ser | Leu | Glu | Asp | Leu | Gln | Asp | Glu | Tyr | Asp | Phe | Lys | Cys | Lys | Thr |
| | | | | 165 | | | | | 170 | | | | | 175 | |

_ Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln
 180 185 190
 Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn
 195 200 205
 Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr
 210 215 220
 Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
 225 230 235 240
 Arg Arg Gln Gln Ser 245 Ala Cys Ile Gly 250 Pro Pro Asn Ala Cys Leu
 255
 Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln
 260 265 270
 Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr
 275 280 285
 Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg
 290 295 300
 Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
 305 310 315 320
 Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
 325 330 335
 Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln
 340 345 350
 Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val
 355 360 365
 Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
 370 375 380
 Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
 385 390 395 400
 Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
 405 410 415
 Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser
 420 425 430
 Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu
 435 440 445
 Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu
 450 455 460
 Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu
 465 470 475 480
 Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala
 485 490 495
 Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg
 500 505 510
 Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly
 515 520 525
 Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys
 530 535 540

Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser
 545 550 555
 Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly
 565 570 575
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys
 580 585 590
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg
 595 600 605
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly
 610 615 620
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser
 625 630 635 640
 Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
 645 650 655
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
 660 665 670
 Lys Asp His Ala Phe Gly Lys Tyr Ser Arg Pro Lys Glu Ala Pro
 675 680 685
 Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr
 690 695 700
 Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr
 705 710 715 720
 Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Val Ser Arg
 725 730 735
 Ile Val Gly Ser Val Glu Phe Asp Ser Met Met Asn Thr Val
 740 745 750

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2607 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 197..2335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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| ATTAAACCTC TCGCGAGGCC C CTCGCGAGA CTCTGCGCCG GAAAGTTTCA TTIGCTGTAT | 60 |
| GCCATCCTCG AGAGCTGTCT AGGTTAACGT TCGCACTCTG TGTATATAAC CTCGACAGTC | 120 |
| TTGGCACCTA ACGTGCTGTG CGTAGCTGCT CCTTGTGTTG AATCCCCAGG CCCTTGTGTTG | 180 |

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|---|------|
| GGCACAAAGGT GGCAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC | 229 |
| Met Ser Gln Trp Tyr Gln Leu Gln Gln Leu Asp | |
| 1 5 10 | |
| TCA AAA TTC CTG GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC | 277 |
| Ser Lys Phe Leu Gln Val His Gln Leu Tyr Asp Ser Phe Pro | |
| 15 20 25 | |
| ATG GAA ATC AGA CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG | 325 |
| Met Glu Ile Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp | |
| 30 35 40 | |
| GAG CAC GCT GCC AAT GAT GTT TCA TTT GCC ACC ATC CGT TTT CAT GAC | 373 |
| Glu His Ala Ala Asn Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp | |
| 45 50 55 | |
| CTC CTG TCA CAG CTG GAT GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT | 421 |
| Leu Leu Ser Gln Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn | |
| 60 65 70 75 | |
| AAC TTC TTG CTA CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG | 469 |
| Asn Phe Leu Leu Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln | |
| 80 85 90 | |
| GAT AAT TTT CAG GAA GAC CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC | 517 |
| Asp Asn Phe Gln Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser | |
| 95 100 105 | |
| TGT CTG AAG GAA GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT | 565 |
| Cys Leu Lys Glu Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn | |
| 110 115 120 | |
| CAG GCT CAG TCG GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG | 613 |
| Gln Ala Gln Ser Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln | |
| 125 130 135 | |
| AAA GAG CTT GAC AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT | 661 |
| Lys Glu Leu Asp Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys | |
| 140 145 150 155 | |
| ATA GAG CAT GAA ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC | 709 |
| Ile Glu His Glu Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp | |
| 160 165 170 | |
| TTC AAA TGC AAA ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG | 757 |
| Phe Lys Cys Lys Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val | |
| 175 180 185 | |
| GCA AAG AGT GAT CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT | 805 |
| Ala Lys Ser Asp Gln Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr | |
| 190 195 200 | |
| TTA ATG CTT GAC AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG | 853 |
| Leu Met Leu Asp Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu | |
| 205 210 215 | |
| TTG CTG AAT GTC ACT GAA CTT ACC CAG AAT GCC CTG ATT AAT GAT GAA | 901 |
| Leu Leu Asn Val Thr Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu | |
| 220 225 230 235 | |
| CTA GTG GAG TGG AAG CGG AGA CAG CAG AGC GCC TGT ATT GGG GGG CCG | 949 |
| Leu Val Glu Trp Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro | |
| 240 245 250 | |
| CCC AAT GCT TGC TTG GAT CAG CTG CAG AAC TGG TTC ACT ATA GTT GCG | 997 |
| Pro Asn Ala Cys Leu Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala | |
| 255 260 265 | |
| GAG AGT CTG CAG CAA GTT CGG CAG CAG CTT AAA AAG TTG GAG GAA TTG | 1045 |

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|---|------|
| Glu Ser Leu Gln Gln Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu | |
| 270 275 280 | |
| GAA CAG AAA TAC ACC TAC GAA CAT GAC CCT ATC ACA AAA AAC AAA CAA | 1093 |
| Glu Gln Lys Tyr Thr Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln | |
| 285 290 295 | |
| GTG TTA TGG GAC CGC ACC TTC AGT CTT TTC CAG CTC ATT CAG AGC | 1141 |
| Val Leu Trp Asp Arg Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser | |
| 300 305 310 315 | |
| TCG TTT GTG GTG GAA AGA CAG CCC TGC ATG CCA ACG CAC CCT CAG AGG | 1189 |
| Ser Phe Val Val Glu Arg Gln Pro Cys Met Thr His Pro Gln Arg | |
| 320 325 330 | |
| CCG CTG GTC TTG AAG ACA GGG GTC CAG TTT ACT GTG AAG TTG AGA CTG | 1237 |
| Pro Leu Val Leu Lys Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu | |
| 335 340 345 | |
| TTG GTG AAA TTG CAA GAG CTG AAT TAT AAT TTG AAA GTC AAA GTC TTA | 1285 |
| Leu Val Lys Leu Gln Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu | |
| 350 355 360 | |
| TTT GAT AAA GAT GTG AAT GAG AGA AAT ACA GTA AAA GGA TTT AGG AAG | 1333 |
| Phe Asp Lys Asp Val Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys | |
| 365 370 375 | |
| TTC AAC ATT TTG GGC ACG CAC ACA AAA GTG ATG AAC ATG GAG GAG TCC | 1381 |
| Phe Asn Ile Leu Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser | |
| 380 385 390 395 | |
| ACC AAT GGC AGT CTG GCG GCT GAA TTT CGG CAC CTG CAA TTG AAA GAA | 1429 |
| Thr Asn Gly Ser Leu Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu | |
| 400 405 410 415 | |
| CAG AAA AAT GCT GGC ACC AGA ACG AAT GAG GGT CCT CTC ATC GTT ACT | 1477 |
| Gln Lys Asn Ala Gly Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr | |
| 415 420 425 430 | |
| GAA GAG CTT CAC TCC CTT AGT TTT GAA ACC CAA TTG TGC CAG CCT GGT | 1525 |
| Glu Glu Leu His Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly | |
| 430 435 440 445 | |
| TTG GTA ATT GAC CTC GAG ACG ACC TCT CTG CCC GTT GTG GTG ATC TCC | 1573 |
| Leu Val Ile Asp Leu Glu Thr Thr Ser Leu Pro Val Val Ile Ser | |
| 445 450 455 460 | |
| AAC GTC AGC CAG CTC CCG AGC GGT TGG GCC TCC ATC CTT TGG TAC AAC | 1621 |
| Asn Val Ser Gln Leu Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn | |
| 460 465 470 475 | |
| ATG CTG GTG GCG GAA CCC AGG AAT CTG TCC TTC TTC CTG ACT CCA CCA | 1669 |
| Met Leu Val Ala Glu Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro | |
| 480 485 490 495 | |
| TGT GCA CGA TGG GCT CAG CTT TCA GAA GTG CTG AGT TGG CAG TTT TCT | 1717 |
| Cys Ala Arg Trp Ala Gln Leu Ser Glu Val Leu Ser Trp Phe Ser | |
| 495 500 505 510 | |
| TCT GTC ACC AAA AGA GGT CTC AAT GTG GAC CAG CTG AAC ATG TTG GGA | 1765 |
| Ser Val Thr Lys Arg Gly Leu Asn Val Asp Gln Leu Met Leu Gly | |
| 510 515 520 525 | |
| GAG AAG CTT CTT GGT CCT AAC GCC AGC CCC GAT GGT CTC ATT CCG TGG | 1813 |
| Glu Lys Leu Leu Gly Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp | |
| 525 530 535 540 | |

| | | | | | | | | | | | | | | | | |
|-------------|------------|------------|-------------|-------------|-------------|-------------|---------|-------------|-------------|-------------|---------|---------|------------|---------|-------------|------|
| ACG Thr 540 | AGG Arg | TTT Phe | TGT Cys | AAG Lys | GAA Glu 545 | AAT Asn | ATA Ile | AAT Asn | GAT Asp | AAA Lys 550 | AAT Asn | TTT Phe | CCC Pro | TTC Phe | TGG Trp 555 | 1861 |
| CTT Leu | TGG Trp | ATT Ile | GAA Glu | AGC Ser 560 | ATC Ile | CTA Leu | GAA Glu | CTC Leu | ATT Ile 565 | AAA Lys | AAA Lys | CAC His | CTG Leu | CTC Glu | CCT Trp 570 | 1909 |
| CTC Leu | TGG Trp | AAT Asn | GAT Asp 575 | GGG Gly | TGC Cys | ATC Ile | ATG Met | GGC Gly 580 | TTC Phe | ATC Ile | AGC Ser | AAG Lys | GAG Glu | CGA Arg | GAG Glu | 1957 |
| CGT Arg | GCC Ala | CTG Leu | TTG Lys 590 | AAG Asp | GAC Gln | CAG Gln | CGG Pro | GGG Gly 595 | ACC Thr | TTC Phe | CTG Leu | CTG Leu | CGG Arg | TTC Phe | | 2005 |
| AGT Ser | GAG Glu | AGC Ser | TCC Ser 605 | CGG Arg | GAA Glu | GGG Gly 610 | GCC Ala | ATC Ile | ACA Thr | TTC Phe | ACA Thr | TGG Trp | GTG Val | GAG Glu | CGG Arg | 2053 |
| TCC Ser | CAG Gln | AAC Asn | GGA Gly 620 | GGC Gly | GAA Glu 625 | CCT Pro | GAC Asp | TTC Phe | CAT His | CGC Ala | GTT Val | GAA Glu | CCC Pro | TAC Tyr | ACG Thr 635 | 2101 |
| AAG Lys | AAA Lys | GAA Glu | CTT Leu 640 | TCT Asp | GCT Ala | GIT Val | ACT Thr | TTC Phe | CCT Asp 645 | GAC Ile | ATC Ile | ATT Arg | CGC Asn | AAT Tyr | TAC Tyr 650 | 2149 |
| AAA Lys | GTC Val | ATG Met | GCT Glu 655 | GCT Ala | GAG Glu | AAT Asn | ATT Ile | CCT Glu 660 | GAG Asn | AAT Pro | CCC Leu | CTG Lys | AAG Tyr | TAT Ser | CTG Leu 665 | 2197 |
| TAT Tyr | CCA Pro | AAT Asn | ATT Ile 670 | GAC Asp | AAA Lys | GAC Asp | CAT His | GCC Ala 675 | TTT Phe | GGA Gly | AAG Lys | TAT Tyr | TAC Tyr | TCC Ser | AGG Arg 680 | 2245 |
| CCA Pro | AAG Lys | GAA Glu | GCA Ala 685 | CCA Pro | GAG Glu | CCA Pro | ATG Met | GAA Glu 690 | CTT Leu | GAT Asp | GGC Gly | CCT Pro | AAA Lys | GGA Gly | ACT Thr 695 | 2293 |
| GGA Gly | TAT Tyr | ATC Ile | AAG Lys 700 | ACT Thr | GAG Glu | TTG Leu | ATT Ile | TCT Ser | GTG Val | TCT Ser | GAA Glu | GTG Val | TAAGTGAACA | | | 2342 |
| CAGAAGAGTG | ACATGTTTAC | AAACCTCAAG | CCAGCCTTGC | TCCTGGCTGG | GGCCTGTTGA | | | | | | | | | | | 2402 |
| AGATGCTTGT | ATTTTACTTT | TCCATTGTAA | TTGTCTATCGC | CATCACAGCT | GAACCTGTTG | | | | | | | | | | | 2462 |
| AGATCCCCGT | GTTACTGCCT | ATCAGCATTT | TACTACTTTA | AAAAAAAAAA | AAAAAGCCAA | | | | | | | | | | | 2522 |
| AAACCAAATT | TGTATTTAAG | GTATATAAAT | TTTCCCAAAA | CTGATACCCCT | TTGAAAAAGT | | | | | | | | | | | 2582 |
| ATAAATAAAA | TGAGCAAAG | TTGAA | | | | | | | | | | | | | | 2607 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Trp | Tyr | Glu | Leu | Gln | Gln | Leu | Asp | Ser | Lys | Phe | Leu | Glu |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | |

Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
 20 25 30
 Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn
 35 40 45
 Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
 50 55 60
 Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
 65 70 75 80
 His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
 85 90 95
 Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu
 100 105 110
 Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly
 115 120 125
 Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
 130 135 140
 Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile
 145 150 155 160
 Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
 165 170 175
 Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln
 180 185 190
 Lys Gln Glu Gln Leu Leu Leu Lys Met Tyr Leu Met Leu Asp Asn
 195 200 205
 Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr
 210 215 220
 Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
 225 230 235 240
 Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
 245 250 255
 Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln
 260 265 270
 Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr
 275 280 285
 Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg
 290 295 300
 Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
 305 310 315
 Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
 325 330 335
 Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln
 340 345 350
 Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val
 355 360 365
 Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
 370 375 380

Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
 385 390 395 400
 Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
 405 410 415
 Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser
 420 425 430
 Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu
 435 440 445
 Glu Thr Thr Ser Leu Pro Val Val Ile Ser Asn Val Ser Gln Leu
 450 455 460
 Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu
 465 470 475 480
 Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala
 485 490 495
 Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg
 500 505 510
 Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly
 515 520 525
 Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys
 530 535 540
 Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser
 545 550 555 560
 Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly
 565 570 575
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys
 580 585 590
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg
 595 600 605
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly
 610 615 620
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser
 625 630 635
 Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
 645 650 655
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
 660 665 670
 Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro
 675 680 685
 Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr
 690 695 700
 Glu Leu Ile Ser Val Ser Glu Val
 705 710

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2277 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mouse
- (vii) IMMEDIATE SOURCE:
(B) CLONE: Murine Stat91
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 5..2251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | | | | | | | | | | | |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CAGG | ATG | TCA | CAG | TGG | TTC | GAG | CTT | CAG | CAG | CTG | GAC | TCC | AAG | TTC | CTG | 49 |
| Met | Ser | Gln | Trp | Phe | Glu | Leu | Gln | Gln | Leu | Asp | Ser | Lys | Phe | Leu | | |
| 1 | | | | | 5 | | | | | 10 | | | | | 15 | |
| GAG | CAG | GTC | CAC | CAG | CTG | TAC | GAT | GAC | AGT | TTC | CCC | ATG | GAA | ATC | AGA | 97 |
| Glu | Gln | Val | His | Gln | Leu | Tyr | Asp | Asp | Ser | Phe | Pro | Met | Glu | Ile | Arg | |
| | | | 20 | | | | | | 25 | | | | | 30 | | |
| CAG | TAC | CTG | GCC | CAG | TGG | CTG | GAA | AAG | CAA | GAC | TGG | GAG | CAC | GCT | GCC | 145 |
| Gln | Tyr | Leu | Ala | Gln | Trp | Leu | Glu | Lys | Gln | Asp | Trp | Glu | His | Ala | Ala | |
| | | | 35 | | | | | 40 | | | | | 45 | | | |
| TAT | GAT | GTC | TCG | TTT | GCG | ACC | ATC | CGC | TTC | CAT | GAC | CTC | CTC | TCA | CAG | 193 |
| Tyr | Asp | Val | Ser | Phe | Ala | Thr | Ile | Arg | Phe | His | Asp | Leu | Leu | Ser | Gln | |
| | | | 50 | | | | 55 | | | | | 60 | | | | |
| CTG | GAC | GAC | CAG | TAC | AGC | CGC | TTT | TCT | CTG | GAG | AAT | AAT | TTC | TTG | TTG | 241 |
| Leu | Asp | Asp | Gln | Tyr | Ser | Arg | Phe | Ser | Leu | Glu | Asn | Asn | Phe | Leu | Leu | |
| | | | 65 | | | 70 | | | | | 75 | | | | | |
| CAG | CAC | AAC | ATA | CGG | AAA | AGC | AAG | CGT | AAT | CTC | CAG | GAT | AAC | TTC | CAA | 289 |
| Gln | His | Asn | Ile | Arg | Lys | Ser | Lys | Arg | Asn | Leu | Gln | Asp | Asn | Phe | Gln | |
| | | | 80 | | | 85 | | | | 90 | | | | | 95 | |
| GAA | GAT | CCC | GTA | CAG | ATG | TCC | ATG | ATC | ATC | TAC | AAC | TGT | CTG | AAG | GAA | 337 |
| Glu | Asp | Pro | Val | Gln | Met | Ser | Met | Ile | Ile | Tyr | Asn | Cys | Leu | Lys | Glu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| GAA | AGG | AAG | ATT | TTG | GAA | AAT | GCC | CAA | AGA | TIT | AAT | CAG | GCC | CAG | GAG | 385 |
| Glu | Arg | Lys | Ile | Leu | Glu | Asn | Ala | Gln | Arg | Phe | Asn | Gln | Ala | Gln | Glu | |
| | | | 115 | | | | 120 | | | | | | 125 | | | |
| GGA | AAT | ATT | CAG | AAC | ACT | GTG | ATG | TTA | GAT | AAA | CAG | AAG | GAG | CTG | GAC | 433 |
| Gly | Asn | Ile | Gln | Asn | Thr | Val | Met | Leu | Asp | Lys | Gln | Lys | Glu | Leu | Asp | |
| | | | 130 | | | | 135 | | | | | 140 | | | | |
| AGT | AAA | GTC | AGA | AAT | GTG | AAG | GAT | CAA | GTC | ATG | TGC | ATA | GAG | CAG | GAA | 481 |
| Ser | Lys | Val | Arg | Asn | Val | Lys | Asp | Gln | Val | Met | Cys | Ile | Glu | Gln | Glu | |
| | | | 145 | | | 150 | | | | | 155 | | | | | |
| ATC | AAG | ACC | CTA | GAA | GAA | TTA | CAA | GAT | GAA | TAT | GAC | TTT | AAA | TGC | AAA | 529 |
| Ile | Lys | Thr | Leu | Glu | Glu | Leu | Gln | Asp | Glu | Tyr | Asp | Phe | Lys | Cys | Lys | |
| | | | | | 165 | | | | | 170 | | | | 175 | | |
| ACC | TCT | CAG | AAC | AGA | GAA | GGT | GAA | GCC | AAT | GGT | GTG | GCG | AAG | AGC | GAC | 577 |
| Thr | Ser | Gln | Asn | Arg | Glu | Gly | Glu | Ala | Asn | Gly | Val | Ala | Lys | Ser | Asp | |
| | | | | 180 | | | | | 185 | | | | | 190 | | |

| | |
|--|------|
| CAA AAA CAG GAA CAG CTG CTG CTC CAC AAG ATG TTT TTA ATG CTT GAC Gln Lys Gln Gln 195 Gln Leu Leu Leu His Lys Met Phe Leu Met Leu Asp | 625 |
| AAT AAG AGA AAG GAG ATA ATT CAC AAA ATC AGA GAG TTG CTG AAT TCC Asn Lys Arg Lys Glu Ile Ile His 210 Lys Ile Arg Glu Leu Asn Ser | 673 |
| ATC GAG CTC ACT CAG AAC ACT CTG ATT AAT GAC GAG CTC GTG GAG TGG Ile Glu Leu Thr Gln Asn Thr 225 Gln Ile Asn Asp Glu Leu Val Glu Trp | 721 |
| AAG CGA AGG CAG CAG AGC GCC TGC ATC GGG GGA CCG CCC AAC GCC TGC Lys Arg Arg Gln Gln Ser 240 Ala Cys Ile Gly Gly 250 Pro Pro Asn Ala Cys | 769 |
| CTG GAT CAG CTG CAA ACG TGG TTC ACC ATT GTT GCA GAG ACC CTG CAG Leu Asp Gln Leu Leu 260 Thr Trp Phe Thr 265 Val Ala Glu Thr Leu Gln | 817 |
| CAG ATC CGT CAG CAG CTT AAA AAG CTG GAG GAG TTG GAA CAG AAA TTC Gln Ile Arg Gln Gln 275 Leu Lys Lys 280 Glu Glu Leu Glu Val Lys Phe | 865 |
| ACC TAT GAG CCC GAC CCT ATT ACA AAA AAC AAG CAG GTG TTG TCA GAT Thr Tyr Glu Pro Asp Pro Ile Thr Lys 290 Lys Asn Lys Gln Val Leu Ser Asp | 913 |
| CGA ACC TTC CTC CTC TTC CAG CAG CTC ATT CAG AGC TCC TTC GTG GTA Arg Thr Phe Leu Leu Phe 310 Gln Gln Leu Ile Gln Ser Ser Phe Val Val | 961 |
| GAA CGA CAG CCG TGC ATG CCC ACT CAC CCG CAG AGG CCC CTG GTC TTG Glu Arg Gln Pro Cys Met 325 Thr His Lys Cys Arg Pro Glu Val Leu | 1009 |
| AAG ACT GGG GTA CAG TTC ACT GTC AAG TCG AGA CTG TTG GTG AAA TTG Lys Thr Gly Val Gln Phe Thr Val Lys 340 Thr Arg Leu Leu Val Lys Leu | 1057 |
| CAA GAG TCG AAT CTA TTA ACG AAA GTG AAA TGT CAC TTT GAC AAA GAT Gln Glu Ser Asn Leu Leu Thr Lys Val Lys Cys His Phe Asp Lys Asp | 1105 |
| GTG AAC GAG AAA AAC ACA GTT AAA GGA TTT CGG AAG TTC ACC ATC TTG Val Asn Glu Lys Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu | 1153 |
| GGT ACG CAC ACA AAA GTG ATG AAC ATG GAA GAA TCC ACC AAC GGA AGT Gly Thr His Thr Lys Val Met 390 Asn Met Glu Glu Ser Thr Asn Gly Ser | 1201 |
| CTG GCA GCT GAG CTC CGA CAC CTG CAA CTG AAG GAA CAG AAA AAC GCT Leu Ala Ala Glu Leu Arg 405 His Leu Gln Leu Lys Glu Gln Lys Asn Ala | 1249 |
| GGG AAC AGA ACT AAT GAG GGG CCT CTC ATT GTC ACC GAA GAA CTT CAC Gly Asn Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His | 1297 |
| TCT CTT AGC TTT GAA ACC CAG TTG TGC CAG CCA GGC TTG GTG ATT GAC Ser Leu Ser Phe Glu Thr Gln Leu Cys 440 Gln Pro Gly Leu Val Ile Asp | 1345 |
| CTG GAG ACC ACC TCT CTT CCT GTC GTG GTG ATC TCC AAC GTC AGC CAG Leu Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln | 1393 |

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| CTC Leu | CCC 465 | AGT Ser | GGC Gly | TGG Trp | GCG Ala | TCT 470 | ATC Ile | CTG Leu | TGG Trp | TAC Tyr | AAC 475 | ATG Met | CTG Leu | GTG Val | ACA Thr | 1441 |
| GAG 480 | CCC Pro | AGG Arg | AAT Asn | CTC Leu | TCC 485 | TTC Phe | TTC Phe | CTG Leu | AAC Asn | CCC 490 | CCG Pro | TGC Cys | GCG Ala | TGG Trp | TGG 495 | 1489 |
| TCC Ser | CAG Gln | CTC Leu | TCA Ser | GAG 500 | GTG Val | TTG Leu | AGT Ser | TGG Trp | CAG 505 | TTT Phe | TCA Ser | TCA Ser | GTC Val | ACC 510 | AAG Lys | 1537 |
| AGA Arg | GGT Gly | CTG Leu | AAC 515 | GCA Ala | GAC Asp | CAG Gln | CTG Leu | AGC 520 | ATG Met | CTG Leu | GGA Gly | GAG Glu | AAG 525 | CTG Leu | CTG Leu | 1585 |
| GGC Gly | CCT Pro | AAT 530 | GCT Ala | GGC Gly | CCT Pro | GAT Asp | GGT 535 | CTT Leu | ATT Ile | CCA Pro | TGG Trp | ACA 540 | AGG Arg | TTT Phe | TGT Cys | 1633 |
| AAG Lys | GAA 545 | AAT Asn | ATT Ile | AAT Asn | GAT Asp | AAA 550 | AAT Asn | TTC Phe | TCC Ser | TTC Phe | TGG 555 | CCT Pro | TGG Trp | ATT Ile | GAC Asp | 1681 |
| ACC Thr | ATC 560 | CTA Leu | GAG Glu | CTC Leu | ATT 565 | AAG Lys | AAC Asn | GAC Asp | CTG Leu | CTG 570 | TGC Cys | CTC Leu | TGG Trp | AAT Asn | GAT 575 | 1729 |
| GGG Gly | TGC Cys | ATT Ile | ATG Met | GGC 580 | TTC Phe | ATC Ile | AGC Ser | AAG Lys | GAG 585 | CGA Arg | GAA Glu | CGC Arg | GCT Ala | CTG 590 | CTC Leu | 1777 |
| AAG Lys | GAC Asp | CAG Gln | CAG Gln | CCA 595 | GGG Pro | ACG Gly | TTC Thr | CTG 600 | CTT Leu | AGA Arg | TTC Phe | AGT Ser | GAG 605 | AGC Ser | TCC Ser | 1825 |
| CGG Arg | GAA 610 | GGG Gly | GCC Ala | ATC Ile | ACA Phe | TTC Thr | ACA 615 | TGG Trp | GTG Val | GAA Glu | CGG Arg | TCC Ser | CAG 620 | AAC Gln | GGA Gly | 1873 |
| GGT Gly | GAA 625 | CCT Pro | GAC Asp | TTC Phe | CAT His | GCC 630 | GTG Ala | GAG Val | CCC Glu | TAC Tyr | ACG 635 | AAA Thr | AAA Lys | GAA Glu | CTT Leu | 1921 |
| TCA Ser | GCT 640 | GTT Val | ACT Thr | TTC Phe | CCA 645 | GAT Pro | ATT Asp | ATT Ile | CGC 650 | AAC Arg | TAC Lys | AAA Tyr | GTC Val | ATG Met | GCT 655 | 1969 |
| GCC Ala | GAG 660 | AAC Glu | ATA Asn | CCA Pro | GAG Glu | AAT Asn | CCC Pro | CTG Leu | AAG 665 | TAT Tyr | CTG Leu | TAC Tyr | CCC Pro | AAT Asn | ATT 670 | 2017 |
| GAC Asp | AAA 675 | GAC Lys | CAC Asp | GCC Ala | TTT Phe | GGG Gly | AAG Lys | TAT 680 | TAT Tyr | TCC Ser | AGA Arg | CCA Pro | AAG 685 | GAA Glu | GCA Ala | 2065 |
| CCA Pro | GAA 690 | CCG Glu | ATG Pro | GAG Met | CTT Glu | GAC Leu | GAC Asp | AAG 695 | CGA Pro | ACT Lys | GGA Arg | TAC Thr | ATC Gly | AAG Tyr | Lys | 2113 |
| ACT Thr | GAG 705 | TTG Glu | ATT Leu | TCT Ser | GTG Val | TCT Ser | GAA 710 | GTC Glu | CAC Val | CCT His | TCT Pro | AGA Ser | CTT Arg | CAG Leu | ACC Thr | 2161 |
| ACA Thr | GAC 720 | AAC Asp | CTG Asn | CTT Leu | CCC Leu | ATG Pro | TCT Met | CCA 725 | GAG Pro | GAG Glu | TTT 730 | GAT Phe | GAG Asp | ATG Glu | TCC Ser | 2209 |

CGG ATA GTG GGC CCC GAA TTT GAC AGT ATG ATG AGC ACA GTA
 Arg Ile Val Gly Pro Glu Phe Asp Ser Met Met Ser Thr Val
 740 745

2251

TAAACACGAA TTTCTCTCTG GCGACA

2277

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Gln Trp Phe Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu
 1 5 10 15
 Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
 20 25 30
 Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Tyr
 35 40 45
 Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
 50 55 60
 Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
 65 70 75 80
 His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
 85 90 95
 Asp Pro Val Gln Met Ser Met Ile Ile Tyr Asn Cys Leu Lys Glu Glu
 100 105 110
 Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Glu Gly
 115 120 125
 Asn Ile Gln Asn Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
 130 135 140
 Lys Val Arg Asn Val Lys Asp Gln Val Met Cys Ile Glu Gln Glu Ile
 145 150 155 160
 Lys Thr Leu Glu Glu Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
 165 170 175
 Ser Gln Asn Arg Glu Gly Glu Ala Asn Gly Val Ala Lys Ser Asp Gln
 180 185 190
 Lys Gln Glu Gln Leu Leu Leu His Lys Met Phe Leu Met Leu Asp Asn
 195 200 205
 Lys Arg Lys Glu Ile Ile His Lys Ile Arg Glu Leu Leu Asn Ser Ile
 210 215 220
 Glu Leu Thr Gln Asn Thr Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
 225 230 235 240
 Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
 245 250 255
 Asp Gln Leu Gln Thr Trp Phe Thr Ile Val Ala Glu Thr Leu Gln Gln
 260 265 270

Ile Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Phe Thr
 275 280 285
 Tyr Glu Pro Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Ser Asp Arg
 290 295 300
 Thr Phe Leu Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
 305 310 315 320
 Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
 325 330 335
 Thr Gly Val Gln Phe Thr Val Lys Ser Arg Leu Leu Val Lys Leu Gln
 340 345 350
 Glu Ser Asn Leu Leu Thr Lys Val Lys Cys His Phe Asp Lys Asp Val
 355 360 365
 Asn Glu Lys Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
 370 375 380
 Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
 385 390 395 400
 Ala Ala Glu Leu Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
 405 410 415
 Asn Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser
 420 425 430
 Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu
 435 440 445
 Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu
 450 455 460
 Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Thr Glu
 465 470 475 480
 Pro Arg Asn Leu Ser Phe Phe Leu Asn Pro Pro Cys Ala Trp Trp Ser
 485 490 495
 Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg
 500 505 510
 Gly Leu Asn Ala Asp Gln Leu Ser Met Leu Gly Glu Lys Leu Leu Gly
 515 520 525
 Pro Asn Ala Gly Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys
 530 535 540
 Glu Asn Ile Asn Asp Lys Asn Phe Ser Phe Trp Pro Trp Ile Asp Thr
 545 550 555 560
 Ile Leu Glu Leu Ile Lys Asn Asp Leu Leu Cys Leu Trp Asn Asp Gly
 565 570 575
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys
 580 585 590
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg
 595 600 605
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly
 610 615 620
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser
 625 630 635 640

Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
645 650 655
Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
660 665 670
Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro
675 680 685
Glu Pro Met Glu Leu Asp Asp Pro Lys Arg Thr Gly Tyr Ile Lys Thr
690 695 700
Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr
705 710 715 720
Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Met Ser Arg
725 730 735
Ile Val Gly Pro Glu Phe Asp Ser Met Met Ser Thr Val
740 745

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mouse
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: splenic/thymic
 - (B) CLONE: Murine 13sfl
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 34...2277
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | |
|--|-----|
| TGCCACTACC TGGACGGAGA GAGAGAGAGC AGC ATG TCT CAG TGG AAT CAA GTC | 54 |
| Met Ser Gln Trp Asn Gln Val | |
| 1 5 | |
| CAA CAA TTA GAA ATC AAG TTT TTG GAG CAA GTA GAT CAG TTC TAT GAT | 102 |
| Gln Gln Leu Glu Ile Lys Phe Leu Glu Gln Val Asp Gln Phe Tyr Asp | |
| 10 15 20 | |
| GAC AAC TTT CCT ATG GAA ATC CGG CAT CTG CTA GCT CAG TGG ATT GAG | 150 |
| Asp Asn Phe Pro Met Glu Ile Arg His Leu Leu Ala Gln Trp Ile Glu | |
| 25 30 35 | |
| ACT CAA GAC TGG GAA GTA GCT TCT AAC AAT GAA ACT ATG GCA ACA ATT | 198 |
| Thr Gln Asp Trp Glu Val Ala Ser Asn Asn Glu Thr Met Ala Thr Ile | |
| 40 45 50 55 | |
| CTG CTT CAA AAC TTA CTA ATA CAA TTG GAT GAA CAG TTG GGG CGG GTT | 246 |
| Leu Leu Gln Asn Leu Leu Ile Gln Leu Asp Glu Gln Leu Gly Arg Val | |
| 60 65 70 | |

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|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| TCC Ser | AAA Lys | GAA Glu | AAA Lys 75 | AAT Asn | CTG Leu | CTA Leu | TTG Leu | ATT Ile 80 | CAC His | AAT Asn | CTA Leu | AAG Lys | AGA Arg 85 | ATT Ile | AGA Arg | 294 |
| AAA Lys | GTT Val | CTT Leu | CAG Gln 90 | GGC Gly | AAG Lys | TTT Phe | CAT His 95 | GGA Gly | AAT Asn | CCA Pro | ATG Met | CAT His 100 | GTA Val | GCT Ala | GTG Val | 342 |
| GTA Val | ATT Ile 105 | TCA Ser | AAT Asn | TGC Cys | TTA Leu | AGG Glu 110 | GAA Glu | GAG Glu | AGG Arg | AGA Arg | ATA Ile 115 | TTG Leu | GCT Ala | GCA Ala | GCC Ala | 390 |
| AAC Asn 120 | ATG Met | CCT Pro | ATC Ile | CAG Gln 125 | GGA Gly | CCT Pro | CTG Leu | GAG Glu | AAA Lys | TCC Ser 130 | TTA Leu | CAG Gln | AGT Ser | TCT Ser | TCA Ser 135 | 438 |
| GTT Val | TCT Ser | GAA Glu | AGA Arg 140 | CAA Gln | AGG Arg | AAT Asn | GTG Val | GAA Glu | CAC His 145 | AAA Lys | GTG Val | TCT Ser | GCC Ala 150 | ATT Ile | AAA Lys | 486 |
| AAC Asn | AGT Ser | GTG Val | CAG Gln 155 | ATG Met | ACA Thr | GAA Glu | CAA Gln | GAT Asp 160 | ACC Thr | AAA Lys | TAC Tyr | TTA Leu | GAA Glu 165 | GAC Asp | CTG Leu | 534 |
| CAA Gln | GAT Asp | GAG Glu | TTT Phe 170 | GAC Asp | TAC Tyr | AGG Arg | TAT Tyr 175 | AAA Lys | ACA Thr | ATT Ile | CAG Gln | ACA Thr 180 | ATG Met | GAT Asp | CAG Gln | 582 |
| GGT Gly 185 | GAC Lys | AAA Lys | AAC Asn | AGT Ser | ATC Ile | CTG Leu 190 | GTG Val | AAC Asn | CAG Gln | GAA Glu | GTT Val 195 | TTG Leu | ACA Thr | CTG Leu | CTG Leu | 630 |
| CAA Gln 200 | GAA Glu | ATG Met | CTT Leu | AAT Asn | AGT Ser 205 | CTG Leu | GAC Asp | TTC Phe | AAG Lys | AGA Lys 210 | AAG Lys | GAA Glu | GCA Ala | CTC Leu | AGT Ser 215 | 678 |
| AAG Lys | ATG Met | ACG Thr | CAG Gln | ATA Ile 220 | GTG Val | AAC Asn | GAG Glu | ACA Thr | GAC Asp 225 | CTG Leu | CTC Leu | ATG Met | AAC Asn | AGC Ser 230 | ATG Met | 726 |
| CTT Leu | CTA Leu | GAA Glu | GAG Glu 235 | CTG Leu | CAG Gln | GAC Asp | TGG Trp | AAA Lys 240 | AAG Lys | CGG Arg | CAC His | AGG Arg 245 | ATT Ile | GCC Ala | TGC Cys | 774 |
| ATT Ile | GGT Gly 250 | GGC Gly | CCG Pro | CTC Leu | CAC His | AAT Asn | GGG Gly 255 | CTG Leu | GAC Gln | CAG Gln | CTT Leu 260 | CAG Gln | AAC Asn | TGC Cys | TTT Phe | 822 |
| ACC Thr 265 | CTA Leu | CTG Leu | GCA Ala | GAG Glu | AGT Ser | CTT Leu 270 | TTC Phe | CAA Gln | CTC Leu | AGA Lys 275 | CAG Gln | CAA Gln | CTG Leu | GAG Glu | AAA Lys | 870 |
| CTA Leu 280 | CAG Gln | GAG Glu | CAA Gln | TCT Ser | ACT Thr 285 | AAA Lys | ATG Met | ACC Thr | TAT Tyr | GAA Glu 290 | GGG Gly | GAT Asp | CCC Pro | ATC Ile | CCT Pro 295 | 918 |
| GCT Ala | CAA Gln | AGA Arg | GCA Ala | CAC His 300 | CTC Leu | CTG Leu | GAA Glu | AGA Arg | GCT Ala 305 | ACC Thr | Phe | CTG Leu | ATC Ile | TAC Tyr | AAC Asn | 966 |
| CTT Leu | TTC Phe | AAG Lys | AAC Asn 315 | TCA Ser | TTT Phe | GTG Val | GTC Val | GAG Glu 320 | CGA Arg | CAC His | GCA Ala | TGC Cys | ATG Met 325 | CCA Pro | ACG Thr | 1014 |
| CAC His | CCT Pro | CAG Gln | AGG Arg 330 | CCG Pro | ATG Met | GTA Val | CTT Leu 335 | AAA Lys | ACC Thr | CTC Leu | ATT Ile | CAG Gln 340 | TTC Phe | ACT Thr | GTA Val | 1062 |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| AAA | CTG | AGA | TTA | CTA | ATA | AAA | TTG | CCG | GAA | CTA | AAC | TAT | CAG | GTG | AAA | 1110 |
| Lys | Leu | Arg | Leu | Leu | Ile | Lys | Leu | Pro | Glu | Leu | Asn | Tyr | Gln | Val | Lys | |
| | 345 | | | | | 350 | | | | | 355 | | | | | |
| GTA | AAG | GCG | TCC | ATT | GAC | AAG | AAT | GTT | TCA | ACT | CTA | AGC | AAT | AGA | AGA | 1158 |
| Val | Lys | Ala | Ser | Ile | Asp | Lys | Asn | Val | Ser | Thr | Leu | Ser | Asn | Arg | Arg | |
| | 360 | | | | 365 | | | | | 370 | | | | | 375 | |
| TTT | GTG | CTT | TGT | GGA | ACT | CAC | GTC | AAA | GCT | ATG | TCC | AGT | GAG | GAA | TCT | 1206 |
| Phe | Val | Leu | Cys | Gly | Thr | His | Val | Lys | Ala | Met | Ser | Ser | Glu | Gln | Ser | |
| | | | | 380 | | | | | 385 | | | | | 390 | | |
| TCC | AAT | GGG | AGC | CTC | TCA | GTG | GAG | TTA | GAC | ATT | GCA | ACC | CAA | GGA | GAT | 1254 |
| Ser | Asn | Gly | Ser | Leu | Ser | Val | Glu | Leu | Asp | Ile | Ala | Thr | His | Gly | Asp | |
| | | | 395 | | | | | 400 | | | | | 405 | | | |
| GAA | GTG | CAG | TAC | TGG | AGT | AAA | GGA | AAC | GAG | GGC | TGC | CAC | ATG | GTG | ACA | 1302 |
| Glu | Val | Gln | Tyr | Trp | Ser | Lys | Gly | Asn | Glu | Gly | Cys | His | Met | Val | Thr | |
| | | 410 | | | | | 415 | | | | | 420 | | | | |
| GAG | GAG | TTG | CAT | TCC | ATA | ACC | TTT | GAG | ACC | CAG | ATC | TGC | CTC | TAT | GGC | 1350 |
| Glu | Glu | Leu | His | Ser | Ile | Thr | Phe | Glu | Thr | Gln | Ile | Cys | Leu | Tyr | Gly | |
| | | 425 | | | | 430 | | | | | 435 | | | | | |
| CTC | ACC | ATT | AAC | CTA | GAG | ACC | AGC | TCA | TTA | CCT | GTC | GTG | ATG | ATT | TCT | 1398 |
| Leu | Thr | Ile | Asn | Leu | Glu | Thr | Ser | Ser | Leu | Pro | Val | Val | Met | Ile | Ser | |
| | | | | 445 | | | | | | 450 | | | | 455 | | |
| AAT | GTC | AGC | CAA | CTA | CCT | AAT | GCA | TGG | GCA | TCC | ATC | ATT | TGG | TAC | AAT | 1446 |
| Asn | Val | Ser | Gln | Leu | Pro | Asn | Ala | Trp | Ala | Ser | Ile | Ile | Trp | Tyr | Asn | |
| | | | | 460 | | | | 465 | | | | | 470 | | | |
| GTA | TCA | ACT | AAC | GAC | TCC | CAG | AAC | TTG | GTT | TTC | TTT | AAT | AAC | CCT | CCA | 1494 |
| Val | Ser | Thr | Asn | Asp | Ser | Gln | Asn | Leu | Val | Phe | Phe | Asn | Asn | Pro | Pro | |
| | | | 475 | | | | | 480 | | | | | 485 | | | |
| TCT | GTC | ACT | TTG | GGC | CAA | CTC | CTG | GAA | GTG | ATG | AGC | TGG | CAA | TTT | TCA | 1542 |
| Ser | Val | Thr | Leu | Gly | Gln | Leu | Leu | Glu | Val | Met | Ser | Trp | Gln | Phe | Ser | |
| | | 490 | | | | | 495 | | | | | 500 | | | | |
| TCC | TAT | GTC | GGT | CGT | GGC | CTT | AAT | TCA | GAG | CAG | CTC | AAC | ATG | CTG | GCA | 1590 |
| Ser | Tyr | Val | Gly | Arg | Gly | Leu | Asn | Ser | Glu | Gln | Leu | Asn | Met | Leu | Ala | |
| | | 505 | | | | 510 | | | | | 515 | | | | | |
| GAG | AAG | CTC | ACA | GTT | CAG | TCT | AAC | TAC | AAT | GAT | GGT | CAC | CTC | ACC | TGG | 1638 |
| Glu | Lys | Leu | Thr | Val | Gln | Ser | Asn | Tyr | Asn | Asp | Gly | His | Leu | Thr | Trp | |
| | | 520 | | | 525 | | | | | 530 | | | | 535 | | |
| GCC | AAG | TTC | TGC | AAG | GAA | CAT | TIG | CCT | GGC | AAA | ACA | TTT | ACC | TTC | TGG | 1686 |
| Ala | Lys | Phe | Cys | Gly | His | Leu | Leu | Pro | Gly | Lys | Thr | Phe | Thr | Phe | Trp | |
| | | | 540 | | | | | | 545 | | | | 550 | | | |
| ACT | TGG | CTT | GAA | GCA | ATA | TTG | GAC | CTA | ATT | AAA | AAA | CAT | ATT | CTT | CCC | 1734 |
| Thr | Trp | Leu | Glu | Ala | Ile | Leu | Asp | Leu | Ile | Lys | Lys | His | Ile | Leu | Pro | |
| | | | 555 | | | | | 560 | | | | | 565 | | | |
| CTC | TGG | ATT | GAT | GGG | TAC | ATC | ATG | GGA | TTT | GTT | AGT | AAA | GAG | AAG | GAA | 1782 |
| Leu | Trp | Ile | Asp | Gly | Tyr | Ile | Met | Gly | Phe | Val | Ser | Lys | Glu | Lys | Glu | |
| | | 570 | | | | | 575 | | | | | 580 | | | | |
| CGG | CTT | CTG | CTC | AAA | GAT | AAA | ATG | CCT | GGG | ACA | TTT | TTG | TTA | AGA | TTC | 1830 |
| Arg | Leu | Leu | Leu | Lys | Asp | Lys | Met | Pro | Gly | Thr | Phe | Leu | Leu | Arg | Phe | |
| | | 585 | | | | 590 | | | | | 595 | | | | | |
| AGT | GAG | AGC | CAT | CTT | GGA | GGG | ATA | ACC | TTC | ACC | TGG | GTG | GAC | CAA | TCT | 1878 |
| Ser | Glu | Ser | His | Leu | Gly | Gly | Ile | Thr | Phe | Thr | Trp | Val | Asp | Gln | Ser | |
| | | 600 | | | 605 | | | | | 610 | | | | | 615 | |

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|--|------|
| GAA AAT GGA GAA GTG AGA TTC CAC TCT GTA GAA CCC TAC AAC AAA GGG Glu Asn Gly Glu Val Arg Phe His Ser Val Glu Pro Tyr Asn Lys Gly | 1926 |
| AGA CTG TCG GCT CTG GCC TTC GCT GAC ATC CTG CGA GAC TAC AAG GTT Arg Leu Ser Ala Leu Ala Phe Ala Asp Ile Leu Arg Asp Tyr Lys Val | 1974 |
| ATC ATG GCT GAA AAC ATC CCT GAA AAC CCT CTG AAG TAC CTC TAC CCT Ile Met Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro | 2022 |
| GAC ATT CCC AAA GAC AAA GCC TTT GGC AAA CAC TAC AGC TCC CAG CCG Asp Ile Pro Lys Asp Lys Ala Phe Gly Lys His Tyr Ser Ser Gln Pro | 2070 |
| TGC GAA GTC TCA AGA CCA ACC GAA CGG GGA GAC AAG GGT TAC GTC CCC Cys Glu Val Ser Arg Pro Thr Glu Arg Gly Asp Lys Gly Tyr Val Pro | 2118 |
| TCT GTT TTT ATC CCC ATT TCA ACA ATC CGA AGC GAT TCC ACG GAG CCA Ser Val Phe Ile Pro Ile Ser Thr Ile Arg Ser Asp Ser Thr Glu Pro | 2166 |
| CAA TCT CCT TCA GAC CTT CTC CCC ATG TCT CCA AGT GCA TAT GCT GTG Gln Ser Pro Ser Asp Leu Leu Pro Met Ser Pro Ser Ala Tyr Ala Val | 2214 |
| CTG AGA GAA AAC CTG AGC CCA ACG ACA ATT GAA ACT GCA ATG AAT TCC Leu Arg Glu Asn Leu Ser Pro Thr Thr Ile Glu Thr Ala Met Asn Ser | 2262 |
| CCA TAT TCT GCT GAA TGACGGTGCA AACGGACACT TTAAGAAGG AAGCAGATGA Pro Tyr Ser Ala Glu | 2317 |
| AACTGGAGAG TGITCTTAC CATAGATCAC AATTATTTC TTCGGCTTG TAAATACC | 2375 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | |
|---|----|----|----|----|
| Met Ser Gln Trp Asn Gln Val Gln Gln Leu Glu Ile Lys Phe Leu Glu | 1 | 5 | 10 | 15 |
| Gln Val Asp Gln Phe Tyr Asp Asp Asn Phe Pro Met Glu Ile Arg His | 20 | 25 | 30 | |
| Leu Leu Ala Gln Trp Ile Glu Thr Gln Asp Trp Glu Val Ala Ser Asn | 35 | 40 | 45 | |
| Asn Glu Thr Met Ala Thr Ile Leu Leu Gln Asn Leu Leu Ile Gln Leu | 50 | 55 | 60 | |
| Asp Glu Gln Leu Gly Arg Val Ser Lys Glu Lys Asn Leu Leu Leu Ile | 65 | 70 | 75 | 80 |
| His Asn Leu Lys Arg Ile Arg Lys Val Leu Gln Gly Lys Phe His Gly | 85 | 90 | 95 | |

Asn Pro Met His Val Ala Val Val Ile Ser Asn Cys Leu Arg Glu Glu
 100 105 110
 Arg Arg Ile Leu Ala Ala Ala Asn Met Pro Ile Gln Gly Pro Leu Glu
 115 120 125
 Lys Ser Leu Gln Ser Ser Ser Val Ser Glu Arg Gln Arg Asn Val Glu
 130 135 140
 His Lys Val Ser Ala Ile Lys Asn Ser Val Gln Met Thr Glu Gln Asp
 145 150 155 160
 Thr Lys Tyr Leu Glu Asp Leu Gln Asp Glu Phe Asp Tyr Arg Tyr Lys
 165 170 175
 Thr Ile Gln Thr Met Asp Gln Gly Asp Lys Asn Ser Ile Leu Val Asn
 180 185 190
 Gln Glu Val Leu Thr Leu Leu Gln Glu Met Leu Asn Ser Leu Asp Phe
 195 200 205
 Lys Arg Lys Glu Ala Leu Ser Lys Met Thr Gln Ile Val Asn Glu Thr
 210 215 220
 Asp Leu Leu Met Asn Ser Met Leu Leu Glu Glu Leu Gln Asp Trp Lys
 225 230 235 240
 Lys Arg His Arg Ile Ala Cys Ile Gly Gly Pro Leu His Asn Gly Leu
 245 250 255
 Asp Gln Leu Gln Asn Cys Phe Thr Leu Leu Ala Glu Ser Leu Phe Gln
 260 265 270
 Leu Arg Gln Gln Leu Glu Lys Leu Gln Glu Gln Ser Thr Lys Met Thr
 275 280 285
 Tyr Glu Gly Asp Pro Ile Pro Ala Gln Arg Ala His Leu Leu Glu Arg
 290 295 300
 Ala Thr Phe Leu Ile Tyr Asn Leu Phe Lys Asn Ser Phe Val Val Glu
 305 310 315 320
 Arg His Ala Cys Met Pro Thr His Pro Gln Arg Pro Met Val Leu Lys
 325 330 335
 Thr Leu Ile Gln Phe Thr Val Lys Leu Arg Leu Leu Ile Lys Leu Pro
 340 345 350
 Glu Leu Asn Tyr Gln Val Lys Val Lys Ala Ser Ile Asp Lys Asn Val
 355 360 365
 Ser Thr Leu Ser Asn Arg Arg Phe Val Leu Cys Gly Thr His Val Lys
 370 375 380
 Ala Met Ser Ser Glu Glu Ser Ser Asn Gly Ser Leu Ser Val Glu Leu
 385 390 395 400
 Asp Ile Ala Thr Gln Gly Asp Glu Val Gln Tyr Trp Ser Lys Gly Asn
 405 410 415
 Glu Gly Cys His Met Val Thr Glu Glu Leu His Ser Ile Thr Phe Glu
 420 425 430
 Thr Gln Ile Cys Leu Tyr Gly Leu Thr Ile Asn Leu Glu Thr Ser Ser
 435 440 445
 Leu Pro Val Val Met Ile Ser Asn Val Ser Gln Leu Pro Asn Ala Trp
 450 455 460

Ala Ser Ile Ile Trp Tyr Asn Val Ser Thr Asn Asp Ser Gln Asn Leu
 465 470 475 480
 Val Phe Phe Asn Asn Pro Pro Ser Val Thr Leu Gly Gln Leu Leu Glu
 485 490 495
 Val Met Ser Trp Gln Phe Ser Ser Tyr Val Gly Arg Gly Leu Asn Ser
 500 505 510
 Glu Gln Leu Asn Met Leu Ala Glu Lys Leu Thr Val Gln Ser Asn Tyr
 515 520 525
 Asn Asp Gly His Leu Thr Trp Ala Lys Phe Cys Lys Glu His Leu Pro
 530 535 540
 Gly Lys Thr Phe Thr Phe Trp Thr Trp Leu Glu Ala Ile Leu Asp Leu
 545 550 555 560
 Ile Lys Lys His Ile Leu Pro Leu Trp Ile Asp Gly Tyr Ile Met Gly
 565 570 575
 Phe Val Ser Lys Glu Lys Glu Arg Leu Leu Lys Asp Lys Met Pro
 580 585 590
 Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser His Leu Gly Gly Ile Thr
 595 600 605
 Phe Thr Trp Val Asp Gln Ser Glu Asn Gly Glu Val Arg Phe His Ser
 610 615 620
 Val Glu Pro Tyr Asn Lys Gly Arg Leu Ser Ala Leu Ala Phe Ala Asp
 625 630 635 640
 Ile Leu Arg Asp Tyr Lys Val Ile Met Ala Glu Asn Ile Pro Glu Asn
 645 650 655
 Pro Leu Lys Tyr Leu Tyr Pro Asp Ile Pro Lys Asp Lys Ala Phe Gly
 660 665 670
 Lys His Tyr Ser Ser Gln Pro Cys Glu Val Ser Arg Pro Thr Glu Arg
 675 680 685
 Gly Asp Lys Gly Tyr Val Pro Ser Val Phe Ile Pro Ile Ser Thr Ile
 690 695 700
 Arg Ser Asp Ser Thr Glu Pro Gln Ser Pro Ser Asp Leu Leu Pro Met
 705 710 715 720
 Ser Pro Ser Ala Tyr Ala Val Leu Arg Glu Asn Leu Ser Pro Thr Thr
 725 730 735
 Ile Glu Thr Ala Met Asn Ser Pro Tyr Ser Ala Glu
 740 745

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2869 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: splenic/thymic

(B) CLONE: Murine 19sf6

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 69..2378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|---|-----|
| GCCGCGACCA GCCAGGCCGG CCAGTCGGGC TCAGCCCGGA GACAGTCGAG ACCCCTGACT | 60 |
| GCAGCAGG ATG GCT CAG TGG AAC CAG CTG CAG CAG CTG GAC ACA CGC TAC | 110 |
| Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr | |
| 1 5 10 | |
| CTG AAG CAG CTG CAC CAG CTG TAC AGC GAC ACG TTC CCC ATG GAG CTG | 158 |
| Leu Lys Gln Leu His Gln Leu Tyr Ser Asp Thr Phe Pro Met Glu Leu | |
| 15 20 25 30 | |
| CGG CAG TTC CTG GCA CCT TGG ATT GAG AGT CAA GAC TGG GCA TAT GCA | 206 |
| Arg Gln Phe Leu Ala Trp Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala | |
| 35 40 45 | |
| GCC AGC AAA GAG TCA CAT GCC ACG TTG GTG TTT CAT AAT CTC TTG GGT | 254 |
| Ala Ser Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly | |
| 50 55 60 | |
| GAA ATT GAC CAG CAA TAT AGC CGA TTC CTG CAA GAG TCC AAT GTC CTC | 302 |
| Glu Ile Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu | |
| 65 70 75 | |
| TAT CAG CAC AAC CTT CGA AGA ATC AAG CAG TTT CTG CAG AGC AGG TAT | 350 |
| Tyr Gln His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr | |
| 80 85 90 | |
| CTT GAG AAG CCA ATG GAA ATT GCC CGG ATC GTG GCC CGA TGC CTG TGG | 398 |
| Leu Glu Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp | |
| 95 100 105 110 | |
| GAA GAG TCT CGC CTC CTC CAG ACG GCA GCC ACG GCA GCC CAG CAA GGG | 446 |
| Glu Glu Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly | |
| 115 120 125 | |
| GGC CAG GCC AAC CAC CCA ACA GCC GCC GTA GTG ACA GAG AAG CAG CAG | 494 |
| Gly Gln Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln | |
| 130 135 140 | |
| ATG TTG GAG CAG CAT CTT CAG GAT GTC CGG AAG CGA GTG CAG GAT CTA | 542 |
| Met Leu Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu | |
| 145 150 155 | |
| GAA CAG AAA ATG AAG GTG GTG GAG AAC CTC CAG GAC GAC TTT GAT TTC | 590 |
| Glu Gln Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe | |
| 160 165 170 | |
| AAC TAC AAA ACC CTC AAG AGC CAA GGA GAC ATG CAG GAT CTG AAT GGA | 638 |
| Asn Tyr Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly | |
| 175 180 185 190 | |
| AAC AAC CAG TCT GTG ACC AGA CAG AAG ATG CAG CAG CTG GAA CAG ATG | 686 |
| Asn Asn Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met | |
| 195 200 205 | |

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|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| CTC Leu | ACA Thr | GCC Ala | CTG Leu 210 | GAC Asp | CAG Gln | ATG Met | CGG Arg | AGA Arg 215 | AGC Ser | ATT Ile | GTG Val | AGT Ser | GAG Glu 220 | CTG Leu | GCG Ala | 734 |
| GGG Gly | CTC Leu | TTG Ser 225 | TCA Ser | GCA Ala | ATG Met | GAG Glu | TAC Tyr 230 | GTG Val | CAG Gln | AAG Lys | ACA Thr | CTG Leu 235 | ACT Thr | GAT Asp | GAA Glu | 782 |
| GAG Glu | CTG Leu | GCT Ala | GAC Asp | TGG Trp | AAG Lys | AGG Arg 245 | CGG Arg | CCA Pro | GAG Glu | ATC Ile | GCG Ala 250 | TGC Cys | ATC Ile | GGA Gly | GGC Gly | 830 |
| CCT Pro 255 | CCC Pro | AAC Asn | ATC Ile | TGC Cys | CTG Leu 260 | GAC Asp | CGT Arg | CTG Leu | GAA Glu | AAC Asn 265 | TGG Trp | ATA Ile | ACT Thr | TCA Ser | TTA Leu 270 | 878 |
| GCA Ala | GAA Glu | TCT Ser | CAA Gln | CTT Leu 275 | CAG Gln | ACC Thr | CGC Arg | CAA Gln 280 | CAA Gln | ATT Ile | AAG Lys | AAA Lys | CTG Leu 285 | GAG Glu | GAG Glu | 926 |
| CTG Leu | CAG Gln | CAG Gln | AAA Lys 290 | GTG Val | TCC Ser | TAC Tyr | AAG Lys | GGC Gly 295 | GAC Asp | CCT Pro | ATC Ile | GTG Val | CAG Gln 300 | CAC His | CGG Arg | 974 |
| CCC Pro | ATG Met | CTG Glu 305 | GAG Glu | GAG Glu | AGG Arg | ATC Ile | GTG Val 310 | GAG Glu | CTG Leu | TTC Phe | AGA Arg | AAC Asn 315 | TTA Leu | ATG Met | AAG Lys | 1022 |
| AGT Ser | GCC Ala | TTC Phe 320 | GTG Val | GTG Val | GAG Glu | CGG Arg 325 | CAG Gln | CCC Pro | TGC Cys | ATG Met | CCC Met 330 | ATG Met | CAC His | CCG Gly | GAC Asp | 1070 |
| CGG Arg 335 | CCC Pro | TTA Leu 340 | GTC Val | ATC Ile | AAG Lys 340 | ACT Thr | GGT Gly | GTC Val | CAG Gln | TTT Phe 345 | ACC Thr | ACG Thr | AAA Lys | GTC Val | AGG Glu 350 | 1118 |
| TTG Leu | CTG Leu | GTC Val | AAA Lys 355 | TTT Phe | CCT Pro | GAG Glu | TTG Leu | AAT Asn | TAT Tyr 360 | CAG Gln | CTT Leu | AAA Lys | ATT Ile | AAA Lys 365 | GTG Val | 1166 |
| TGC Cys | ATT Ile | GAT Asp | AAA Lys 370 | GAC Asp | TCT Ser | GGG Gly | GAT Asp | GTT Val | GCT Ala | GCC Ala | CTC Leu | AGA Arg | GGG Gly | TCT Ser | CGG Arg | 1214 |
| AAA Lys | TTT Phe | AAC Asn 385 | ATT Ile | CTG Leu | GGC Gly | ACG Thr | AAC Asn 390 | ACA Thr | AAA Lys | GTG Val | ATG Met | AAC Asn 395 | ATG Met | GAG Glu | GAG Glu | 1262 |
| TCT Ser | AAC Asn | AAC Asn 400 | GGC Gly | AGC Ser | CTG Leu | TCT Ser 405 | GCA Ala | GAG Glu | TTC Phe | AAG Lys | CAC His 410 | CTG Leu | ACC Thr | CTT Leu | AGG Arg | 1310 |
| GAG Glu 415 | CAG Gln | AGA Arg | TGT Cys | GGG Gly | AAT Gly 420 | GGA Gly | GGC Gly | CGT Arg | GCC Ala | AAT Gly 425 | TGT Cys | GAT Asp | GCC Ala | TCC Ser | TTG Leu 430 | 1358 |
| ATC Ile | GTG Val | ACT Thr | GAG Glu 435 | GAG Leu | CTG His | CAC Leu | CTG Leu | ATC Ile | ACC Thr 440 | TTC Phe | GAG Glu | ACT Thr | GAG Glu | GTG Val 445 | TAC Tyr | 1406 |
| CAC His | CAA Gln | GGC Gly | CTC Leu 450 | AAG Lys | ATT Ile | GAC Asp | CTA Leu | GAG Glu 455 | ACC Thr | CAC His | TCC Ser | TTG Leu | CCA Pro 460 | GTT Val | GTG Val | 1454 |
| GTG Val | ATC Ile | TCC Ser 465 | AAC Asn | ATC Ile | TGT Cys | CAG Gln | ATG Met 470 | CCA Pro | AAT Asn | GCT Ala | TGG Trp | GCA Ala | TCA Ser | ATC Ile | CTG Leu | 1502 |

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| TGG Trp | TAT Tyr 480 | AAC Asn | ATG Met | CTG Leu | ACC Thr | AAT Asn 485 | AAC Asn | CCC Pro | AAG Lys | AAC Asn | GTG Val 490 | AAC Asn | TTC Phe | TTC Phe | ACT Thr | 1550 |
| AAG Lys 495 | CCG Pro | CCA Pro | ATT Ile | GGA Gly 500 | ACC Thr | TGG Trp | GAC Asp | CAA Gln | GTG Val | GCC Ala 505 | GAG Glu | GTG Val | CTC Leu | AGC Ser | TGG Trp 510 | 1598 |
| CAG Gln | TTC Phe | TCG Ser | TCC Ser | ACC Thr 515 | ACC Thr | AAG Lys | CGA Arg | GGG Gly | CTG Leu 520 | AGC Ser | ATC Ile | GAG Glu | CAG Gln | CTG Leu 525 | ACA Thr | 1646 |
| ACG Thr | CTG Leu | GCT Ala 530 | GAG Glu | AAG Lys | CTC Leu | CTA Leu | GGG Gly | CCT Pro 535 | GGT Gly | GTG Val | AAC Asn | TAC Tyr | TCA Ser 540 | GGG Gly | TGT Cys | 1694 |
| CAG Gln | ATC Ile | ACA Ile 545 | TGG Trp | GCT Ala | AAA Lys | TTC Phe | TGC Cys 550 | AAA Lys | GAA Glu | AAC Asn | ATG Met | GCT Ala 555 | GGC Gly | AAG Lys | GGC Gly | 1742 |
| TTC Phe | TCC Phe 560 | TTC Phe | TGG Trp | GTC Val | TGG Trp | CTA Leu 565 | GAC Asp | AAT Asn | ATC Ile | ATC Ile | GAC Leu 570 | CTT Leu | GTG Val | AAA Lys | AAG Lys | 1790 |
| TAT Tyr 575 | ATC Ile | TTG Leu | GCC Ala | CTT Leu | TGG Trp 580 | AAT Asn | GAA Glu | GGG Gly | TAC Tyr | ATC Ile 585 | ATG Met | GGT Gly | TTC Phe | ATC Ile | AGC Ser 590 | 1838 |
| AAG Lys | GAG Glu | CGG Arg | GAG Glu | CGG Arg 595 | GCC Ala | ATC Ile | CTA Leu | AGC Ser | ACA Glu 600 | AAG Lys | CCC Pro | CCG Pro | GGC Gly 605 | ACC Phe | TTC Phe | 1886 |
| CTA Leu | CTG Leu | CGC Arg 610 | TTC Phe | AGC Ser | GAG Glu | AGC Ser | AGC Ser | AAA Lys 615 | GAA Glu | GGA Gly | GGG Gly | GTC Val | ACT Thr 620 | TTC Phe | ACT Thr | 1934 |
| TGG Trp | GTG Val | GAA Glu 625 | AAG Lys | GAC Asp | ATC Ile | AGT Ser | GGC Gly 630 | AAG Lys | ACC Thr | CAG Gln | ATC Ile 635 | CAG Gln | TCT Ser | GTA Val | GAG Glu | 1982 |
| CCA Pro | TAC Tyr 640 | ACC Thr | AAG Lys | CAG Gln | CAG Gln | CTG Leu 645 | AAC Asn | AAC Asn | ATG Met | TCA Ser | TTT Phe 650 | GCT Ala | GAA Glu | ATC Ile | ATC Ile | 2030 |
| ATG Met 655 | GGC Gly | TAT Tyr | AAG Lys | ATC Ile | ATG Met 660 | GAT Asp | GCG Ala | ACC Thr | AAC Asn 665 | ATC Ile | CTG Leu | GTG Val | TCT Ser | CCA Pro | CTT Leu 670 | 2078 |
| GTC Val | TAC Tyr | CTC Leu | TAC Tyr | CCC Pro 675 | GAC Asp | ATT Thr | CCC Pro | AAG Pro | GAG Glu 680 | GAG Glu | GCA Ala | TTT Phe | GGA Gly 685 | AAG Lys | TAC Thr | 2126 |
| TGT Cys | AGG Arg | CCC Pro 690 | GAG Glu | AGC Ser | CAG Glu | GAG Glu | CAC His | CCC Pro 695 | GAA Glu | GCC Ala | GAC Asp | CCA Pro | GGT Gly 700 | AGT Ser | GCT Ala | 2174 |
| GCC Ala | CCG Pro | TAC Tyr 705 | CTG Leu | AAG Lys | ACC Thr | AAG Lys | TTC Phe 710 | ATC Met | TGT Cys | GTG Val | ACA Thr 715 | CCA Pro | ACG Thr | ACC Thr | TGC Cys | 2222 |
| AGC Ser | AAT Asn | ACC Thr | ATT Ile | GAC Asp | CTG Leu | CCG Pro 725 | ATG Met | TCC Ser | CCC Pro | CGC Arg | ACT Thr 730 | TTA Leu | GAT Asp | TCA Ser | TTG Leu | 2270 |
| ATG Met 735 | CAG Gln | TTT Phe | GGA Gly | AAT Asn | AAC Asn 740 | GGT Gly | GAA Glu | GGT Gly | GCT Ala | GAG Glu 745 | CCC Pro | TCA Ser | GCA Ala | GGA Gly | GGG Gly 750 | 2318 |

| | |
|--|------|
| CAG TTT GAG TCG CTC ACG TTT GAC ATG GAT CTG ACC TCG GAG TGT GCT | 2366 |
| Gln Phe Glu Ser Leu Thr Phe Asp Met Asp Leu Thr Ser Glu Cys Ala | |
| 755 760 765 | |
| ACC TCC CCC ATG TGAGGAGCTG AAACCAGAAG CTGCAGAGAC GTGACTTGAG | 2418 |
| Thr Ser Pro Met | |
| 770 | |
| ACACCTGCCC CGTGCTCCAC CCCTAAGCAG CCGAACCCCA TATCGTCTGA AACTCCTAAC | 2478 |
| TTTGTGGTTC CAGATTTTTT TTTTAAATTT CCTACTTCTG CTATCTTTGG GCAATCTGGG | 2538 |
| CACITTTTAA AAGAGAGAAA TGAGTGAGTG TGGGTGATAA ACTGTTATGT AAAGAGGAGA | 2598 |
| GACCTCTGAG TCTGGGGATG GGGCTGAGAG CAGAAGGGAG GCAAAGGGGA ACACCTCCTG | 2658 |
| TCCTGCCCGC CTGCCCTCCT TTTTCAGCAG CTCGGGGGTT GGTGTGTTAGA CAAGTGCCTC | 2718 |
| CTGGTGCCCA TGGCTACCTG TTGCCCCACT CTGTGAGCTG ATACCCCATC CTGGGAACCTC | 2778 |
| CTGGCTCTGC ACTTTCAACC TTGCTAATAT CCACATAGAA GCTAGGACTA AGCCCAAGGAG | 2838 |
| GTTCTCTTTT AAATTAAAAA AAAAAAAAAA A | 2869 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gln | Trp | Asn | Gln | Leu | Gln | Gln | Leu | Asp | Thr | Arg | Tyr | Leu | Lys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gln | Leu | His | Gln | Leu | Tyr | Ser | Asp | Thr | Phe | Pro | Met | Glu | Leu | Arg | Gln |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Leu | Ala | Pro | Trp | Ile | Glu | Ser | Gln | Asp | Trp | Ala | Tyr | Ala | Ala | Ser |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Lys | Glu | Ser | His | Ala | Thr | Leu | Val | Phe | His | Asn | Leu | Leu | Gly | Glu | Ile |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Asp | Gln | Gln | Tyr | Ser | Arg | Phe | Leu | Gln | Glu | Ser | Asn | Val | Leu | Tyr | Gln |
| | 65 | | | | 70 | | | | | 75 | | | | 80 | |
| His | Asn | Leu | Arg | Arg | Ile | Lys | Gln | Phe | Leu | Gln | Ser | Arg | Tyr | Leu | Glu |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Lys | Pro | Met | Glu | Ile | Ala | Arg | Ile | Val | Ala | Arg | Cys | Leu | Trp | Glu | Glu |
| | | | 100 | | | | 105 | | | | | | 110 | | |
| Ser | Arg | Leu | Leu | Gln | Thr | Ala | Ala | Thr | Ala | Ala | Gln | Gln | Gly | Gly | Gln |
| | | 115 | | | | 120 | | | | | 125 | | | | |
| Ala | Asn | His | Pro | Thr | Ala | Ala | Val | Val | Thr | Glu | Lys | Gln | Gln | Met | Leu |
| | 130 | | | | 135 | | | | | | 140 | | | | |
| Glu | Gln | His | Leu | Gln | Asp | Val | Arg | Lys | Arg | Val | Gln | Asp | Leu | Glu | Gln |
| | 145 | | | | 150 | | | | | 155 | | | | 160 | |
| Lys | Met | Lys | Val | Val | Glu | Asn | Leu | Gln | Asp | Asp | Phe | Asp | Phe | Asn | Tyr |
| | | | 165 | | | | | | 170 | | | | | 175 | |

Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly Asn Asn
 180 185 190
 Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr
 195 200
 Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala Gly Leu
 210 215 220
 Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Leu Thr Asp Glu Glu Leu
 225 230 235 240
 Ala Asp Trp Lys Arg Arg Pro Glu Ile Ala Cys Ile Gly Gly Pro Pro
 245 250 255
 Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu Ala Glu
 260 265 270
 Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu Leu Gln
 275 280 285
 Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met
 290 295 300
 Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala
 305 310 315 320
 Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp Arg Pro
 325 330 335
 Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg Leu Leu
 340 345 350
 Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val Cys Ile
 355 360 365
 Asp Lys Asp Ser Gly Asp Val Ala Ala Leu Arg Gly Ser Arg Lys Phe
 370 375 380
 Asn Ile Leu Gly Thr Asn Thr Lys Val Met Asn Met Glu Glu Ser Asn
 385 390 395 400
 Asn Gly Ser Leu Ser Ala Glu Phe Lys His Leu Thr Leu Arg Glu Gln
 405 410 415
 Arg Cys Gly Asn Gly Gly Arg Ala Asn Cys Asp Ala Ser Leu Ile Val
 420 425 430
 Thr Glu Glu Leu His Leu Ile Thr Phe Glu Thr Glu Val Tyr His Gln
 435 440 445
 Gly Leu Lys Ile Asp Leu Glu Thr His Ser Leu Pro Val Val Val Ile
 450 455 460
 Ser Asn Ile Cys Gln Met Pro Asn Ala Trp Ala Ser Ile Leu Trp Tyr
 465 470 475 480
 Asn Met Leu Thr Asn Asn Pro Lys Asn Val Asn Phe Phe Thr Lys Pro
 485 490 495
 Pro Ile Gly Thr Trp Asp Gln Val Ala Glu Val Leu Ser Trp Gln Phe
 500 505 510
 Ser Ser Thr Thr Lys Arg Gly Leu Ser Ile Glu Gln Leu Thr Thr Leu
 515 520 525
 Ala Glu Lys Leu Leu Gly Pro Gly Val Asn Tyr Ser Gly Cys Gln Ile
 530 535 540

Thr Trp Ala Lys Phe Cys Lys Glu Asn Met Ala Gly Lys Gly Phe Ser
 545 550 555
 Phe Trp Val Trp Leu Asp Asn Ile Ile Asp Leu Val Lys Lys Tyr Ile
 565 570 575
 Leu Ala Leu Trp Asn Glu Gly Tyr Ile Met Gly Phe Ile Ser Lys Glu
 580 585 590
 Arg Glu Arg Ala Ile Leu Ser Thr Lys Pro Pro Gly Thr Phe Leu Leu
 595 600 605
 Arg Phe Ser Glu Ser Ser Lys Glu Gly Gly Val Thr Phe Thr Trp Val
 610 615 620
 Glu Lys Asp Ile Ser Gly Lys Thr Gln Ile Gln Ser Val Glu Pro Tyr
 625 630 635 640
 Thr Lys Gln Gln Leu Asn Asn Met Ser Phe Ala Glu Ile Ile Met Gly
 645 650 655
 Tyr Lys Ile Met Asp Ala Thr Asn Ile Leu Val Ser Pro Leu Val Tyr
 660 665 670
 Leu Tyr Pro Asp Ile Pro Lys Glu Glu Ala Phe Gly Lys Tyr Cys Arg
 675 680 685
 Pro Glu Ser Gln Glu His Pro Glu Ala Asp Pro Gly Ser Ala Ala Pro
 690 695 700
 Tyr Leu Lys Thr Lys Phe Ile Cys Val Thr Pro Thr Thr Cys Ser Asn
 705 710 715 720
 Thr Ile Asp Leu Pro Met Ser Pro Arg Thr Leu Asp Ser Leu Met Gln
 725 730 735
 Phe Gly Asn Asn Gly Glu Gly Ala Glu Pro Ser Ala Gly Gly Gln Phe
 740 745 750
 Glu Ser Leu Thr Phe Asp Met Asp Leu Thr Ser Glu Cys Ala Thr Ser
 755 760 765
 Pro Met
 770

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAAYACNGARC CNATGGARAT YATT

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAYGTNGAYC ARYTNAAYAT G

21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

RTCDATRTTN GRGTANAR

18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTAYAANTYR AYCAGNGYAA

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATCGAGATG TATTCCCAG AAAAG

25

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr Glu Leu Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly Tyr Ile Lys Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys Val Asn Leu Gln Glu Arg Arg Lys Tyr Leu Lys His Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Glu Pro Gln Tyr Glu Glu Ile Pro Ile Tyr Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Src

- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Waksman, et al.

(C) JOURNAL: Nature
 (D) VOLUME: 358
 (F) PAGES: 646-653
 (G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg
 1 5 10 15
 Leu Leu Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu
 20 25 30
 Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Phe
 35 40 45
 Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu
 50 55 60
 Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu
 65 70 75 80
 Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His
 85 90 95
 Arg Leu Thr Asn Val Cys Pro Thr Ser
 100 105

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: Abl

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Overduin, et al.
 (C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
 (D) VOLUME: 89
 (F) PAGES: 11673-11677
 (G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Lys His Ser Trp Tyr His Gly Pro Val Ser Arg Asn Ala Ala Glu
 1 5 10 15
 Tyr Leu Leu Ser Ser Gly Ile Asn Gly Ser Phe Leu Val Arg Glu Ser
 20 25 30
 Asp Arg Arg Pro Gly Gln Arg Ser Ile Ser Leu Arg Tyr Glu Glu Gly
 35 40 45
 Arg Val Tyr His Tyr Arg Ile Asn Thr Ala Ser Asp Gly Lys Leu Tyr
 50 55 60

Val Ser Ser Glu Ser Arg Phe Asn Thr Leu Ala Glu Leu Val His His
65 70 75 80
His Ser Thr Val Ala Asp Gly Leu Ile Thr Thr Leu His Tyr Pro Ala
85 90 95
Pro Lys Arg

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Lck
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Eck, et al.
 - (C) JOURNAL: Nature
 - (D) VOLUME: 362
 - (F) PAGES: 87-91
 - (G) DATE: 1993
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp Phe Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu
1 5 10 15
Ala Pro Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser
20 25 30
Thr Ala Gly Ser Phe Ser Leu Ser Val Arg Asp Asp Phe Asp Gln Asn
35 40 45
Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly
50 55 60
Gly Phe Tyr Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Asp Leu
65 70 75 80
Val Arg His Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser
85 90 95
Arg Pro Cys Gln Thr Gln
100

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:25:

Gln Asp Ala Glu Trp Tyr Trp Gly Asp Ile Ser Arg Glu Glu Val Asn
1 5 10 15

Glu Lys Leu Arg Asp Thr Ala Asp Gly Thr Phe Leu Val Arg Asp Ala
20 25 30

Ser Thr Lys Met His Gly Asp Tyr Thr Leu Thr Leu Arg Lys Gly Gly
35 40 45

Asn Asn Lys Leu Ile Lys Ile Phe His Arg Asp Gly Lys Tyr Gly Phe
50 55 60

Ser Asp Pro Leu Thr Phe Asn Ser Val Val Glu Leu Ile Asn His Tyr
65 70 75 80

Arg His Glu Ser Leu Ala Gln Tyr Asn Pro Lys Leu Asp Val Lys Leu
85 90 95

Leu Tyr Pro